

SEQUENCE LISTING

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DT04 Rec'd PCT/PTO 05 OCT 2004

<110> Jørgensen, Steen Troels  
Olsen, Peter Bjarke  
Andersen, Jens Tønne  
Rasmussen, Michael Dolberg

<120> Improved Bacillus Host Cell

<130> 10295.204-US

<160> 191

<170> PatentIn version 3.3

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<212> DNA

<213> Bacillus licheniformis

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His Leu Glu Ala Leu Ala Glu Lys Pro Ala Lys Val Gln Ile Gln Leu
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Glu Lys Val Tyr Leu Asp Gly Asp Val Gly Ile Glu Asn Lys Val Glu
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Leu Phe Arg Lys Gln Val Asp Asp Ile Ser Pro Leu Ser Lys Thr Asn  
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Gly Tyr Ile Gly Val Thr Glu Asp Gly Val Ile Ser Thr Phe His Gly  
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Leu Pro Asp Arg His Phe Leu Pro Val Asp His Thr Leu His Asp Asp				
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Gly His His Glu His Glu Val Lys Thr Val Val His Leu His Gly Gly				
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Cys Thr Pro Ala Asp Ser Asp Gly Tyr Pro Glu Ala Trp Tyr Thr Lys				
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Ser Ser Leu Pro Arg Ile Leu Arg Lys Arg Pro Phe Tyr Arg Arg His	
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Tyr Gly Arg Pro Val Leu Leu Leu Asn Asn Thr Lys Trp His Glu Pro	
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Val Thr Glu Thr Pro Ala Leu Gly Ser Thr Glu Ile Trp Ser Ile Ile	
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Asn Ala Gly Arg Ala Ile His Pro Ile His Leu His Leu Val Gln Phe	
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Gly Glu Leu Val Phe Thr Gly Pro Ala Val Pro Pro Ala Pro Asn Glu	
445 450 455	

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 35 40 45

Phe Gly Tyr Asn Gly Val Tyr Pro Gly Pro Thr Phe Glu Val Gln Lys  
 50 55 60

His Glu Lys Val Ala Val Lys Trp Leu Asn Lys Leu Pro Asp Arg His  
 65 70 75 80

Phe Leu Pro Val Asp His Thr Leu His Asp Asp Gly His His Glu His  
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Glu Val Lys Thr Val Val His Leu His Gly Gly Cys Thr Pro Ala Asp  
 100 105 110

Ser Asp Gly Tyr Pro Glu Ala Trp Tyr Thr Lys Asp Phe His Ala Lys

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Glu Arg Ser Leu Asn Leu Pro Lys Gly Glu Tyr Glu Ile Pro Leu Leu 180 185 190		
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Gln Pro Asp Asn Pro Ser Pro Asp Leu Pro Asp Pro Ser Ile Val Pro 210 215 220		
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 385 390 395 400

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Arg Pro Phe Asp Ile Glu Arg Tyr Gln Glu Asn Gly Glu Leu Val Phe  
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Thr Gly Pro Ala Val Pro Pro Ala Pro Asn Glu Lys Gly Leu Lys Asp  
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Thr Val Lys Val Pro Pro Gly Ser Val Thr Arg Ile Ile Ala Thr Phe  
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Asn	Pro	Glu	Phe	Leu	Val	Gly	Asp	Pro	Glu	Glu						
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Lys Ile Gly Lys Thr Val Glu Ile Glu Gly Thr Tyr Asp Ile Asn Val  
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Trp Tyr Ser Tyr Ala Asp Asn Thr Lys Thr Glu Val Val Thr Glu Arg  
65 70 75 80

Val Ser Tyr Val Asp Val Ile Lys Leu Arg Tyr Arg Asp Lys Asn Tyr  
85 90 95

Leu Asp Asp Glu His Glu Val Ile Ala Lys Val Leu Gln Gln Pro Asn  
100 105 110

Cys Leu Glu Val Thr Ile Ser Pro Asn Gly Asn Lys Val Val Val Gln  
115 120 125

Ala Glu Arg Glu Phe Leu Ala Glu Val Val Gly Glu Thr Lys Val Val  
130 135 140

Val Glu Val Asn Ser Asp Trp Thr Glu Ser Asp Glu Glu Glu Ala Trp  
145 150 155 160

Glu Glu Glu Leu Asp Glu Glu Leu Glu Asp Ile Asn Pro Glu Phe Leu  
165 170 175

Val Gly Asp Pro Glu Glu



<210> 9  
 <211> 1477  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(974)

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<400> 9
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tctttattct aacataaggt caaatcgcaa gtaaaacgat cataaggctt gaaagcgagc      180
gaatgttcca tgtgaaacag tgtcagtcga gaaaccccgga tttttcttta tttttctttc      240
tcgcctttct gatcagcaac aatataatca aaactgcgac cagaagcgtc acgcaagcc      300
ctccgctcaa aaatagaaaa aagtccttca acatatccaa cacattgatc acctctcact      360
gttgtcactt agatgcaaaa atccccgtatt atttgacttc ccctttccaa aacgggtctaa      420
aacgtccctc agattcttct taacctttag acggtaatgg gcatatgctg actaagaaaa      480
agcaataaag gagaatatga atg aca aca aaa aca ttg gct tgg cat gaa acg      533
                Met Thr Thr Lys Thr Leu Ala Trp His Glu Thr
                  1             5             10

ttg gag ttg cat gaa cta atc gcg gca cag tct gtc gga ttg gtg aag      581
Leu Glu Leu His Glu Leu Ile Ala Ala Gln Ser Val Gly Leu Val Lys
                15             20             25

atc aag aaa agc atg aag aaa atc agc gac cct cag tta aga cag ctt      629
Ile Lys Lys Ser Met Lys Lys Ile Ser Asp Pro Gln Leu Arg Gln Leu
                30             35             40

tac agc gtg tca gca aaa gca ttg gag caa aat tta aga gag ctt ctt      677
Tyr Ser Val Ser Ala Lys Ala Leu Glu Gln Asn Leu Arg Glu Leu Leu
                45             50             55

ccc ttt ttg cca aaa gct cca gca ttt cag cgg gag gat gaa cgg gct      725
Pro Phe Leu Pro Lys Ala Pro Ala Phe Gln Arg Glu Asp Glu Arg Ala
        60             65             70             75

gac ttg tat ttt gat gcg ggt gat ctg ttg gtg ctg gcg aaa acg acc      773
Asp Leu Tyr Phe Asp Ala Gly Asp Leu Leu Val Leu Ala Lys Thr Thr
                80             85             90

gtt cga aac tat gcg att gcg atc acg gaa acg gcg acg ccc gag ctc      821
Val Arg Asn Tyr Ala Ile Ala Ile Thr Glu Thr Ala Thr Pro Glu Leu
                95             100            105

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agg aga gtg ctt gtt aaa caa atc aat gcg gcc att aag ttg cat gaa 869  
 Arg Arg Val Leu Val Lys Gln Ile Asn Ala Ala Ile Lys Leu His Glu  
 110 115 120

caa gtt ttt tat ttt atg tac caa aga ggc tta tat ccc gcc tat aac 917  
 Gln Val Phe Tyr Phe Met Tyr Gln Arg Gly Leu Tyr Pro Ala Tyr Asn  
 125 130 135

ctc gtc gac ctg cta aaa ggc gac gcc atg cat gcg caa aaa gcg ata 965  
 Leu Val Asp Leu Leu Lys Gly Asp Ala Met His Ala Gln Lys Ala Ile  
 140 145 150 155

tcg atg aga taaaaaagcc agcgaggata gaatcctcac tggctctgtt 1014  
 Ser Met Arg

ttttgctatt ttacgattaa aaccggacac ttcactcttt tcgccacttt atggctgaca 1074

cttccgagca ccatttcctg caaagtgttc agccccctgc ttccgataat cacgatatca 1134

acatcatgat ggttggcgta cgatacaatg gccggggcccg gatccccgtg ctgcatcgtc 1194

atttgatagg gaacggccgc ctgttttaaat ttatttttcta tcgacagcag cctgctgcgc 1254

cgttcgcgtt cgagttctgt acgggttttcg ctatgcagga cttcatgttt tgctctcgca 1314

taatccaata cataaatcat gtcgacgacc gtttcgtttg acatggaagc cagatgaatc 1374

gcatgatcgg cagctctttc agaatgcttg gaaccgtcag cagccagcag tatatgtcta 1434

tacacccttc atcacccggt tcttagtgat ttgacactga acg 1477

<210> 10

<211> 158

<212> PRT

<213> Bacillus licheniformis

<400> 10

Met Thr Thr Lys Thr Leu Ala Trp His Glu Thr Leu Glu Leu His Glu  
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Leu Ile Ala Ala Gln Ser Val Gly Leu Val Lys Ile Lys Lys Ser Met  
 20 25 30

Lys Lys Ile Ser Asp Pro Gln Leu Arg Gln Leu Tyr Ser Val Ser Ala  
 35 40 45

Lys Ala Leu Glu Gln Asn Leu Arg Glu Leu Leu Pro Phe Leu Pro Lys  
 50 55 60

Ala Pro Ala Phe Gln Arg Glu Asp Glu Arg Ala Asp Leu Tyr Phe Asp  
65 70 75 80

Ala Gly Asp Leu Leu Val Leu Ala Lys Thr Thr Val Arg Asn Tyr Ala  
85 90 95

Ile Ala Ile Thr Glu Thr Ala Thr Pro Glu Leu Arg Arg Val Leu Val  
100 105 110

Lys Gln Ile Asn Ala Ala Ile Lys Leu His Glu Gln Val Phe Tyr Phe  
115 120 125

Met Tyr Gln Arg Gly Leu Tyr Pro Ala Tyr Asn Leu Val Asp Leu Leu  
130 135 140

Lys Gly Asp Ala Met His Ala Gln Lys Ala Ile Ser Met Arg  
145 150 155

<210> 11  
<211> 1752  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (183)..(1256)

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cggctctgctt ccgggacagg tttttttcac atatgatatg tcagctgaaa aaggaggaaa 180  
tg atg atg agt gcc act gcc ttg ccg gcc ttt agg ctg cac att cat 227  
Met Met Ser Ala Thr Ala Leu Pro Ala Phe Arg Leu His Ile His  
1 5 10 15  
ccg aag cat ctg ctt gag ttg aaa aaa gac gtc tgg agt gat gaa gcc 275  
Pro Lys His Leu Leu Glu Leu Lys Lys Asp Val Trp Ser Asp Glu Ala  
20 25 30  
gtt ccc ggc atg ctc ttg acc ggt tca gca aag acg cct gtc gca gtg 323  
Val Pro Gly Met Leu Leu Thr Gly Ser Ala Lys Thr Pro Val Ala Val  
35 40 45  
tca tac aga ggg gcc cac acc cgc aaa ctg acg aaa aaa tcc tat ttc 371  
Ser Tyr Arg Gly Ala His Thr Arg Lys Leu Thr Lys Lys Ser Tyr Phe  
50 55 60

att caa tat ccg gac aat aaa gaa aag gct gcg ttt cat ttg aac gcg Ile Gln Tyr Pro Asp Asn Lys Glu Lys Ala Ala Phe His Leu Asn Ala 65 70 75	419
gaa tat cat gat ccg tct ttc atc aga aac agg ctt tcc ttt cat ttt Glu Tyr His Asp Pro Ser Phe Ile Arg Asn Arg Leu Ser Phe His Phe 80 85 90 95	467
ttt gaa caa atc ggc gtc ctt gcg cca gca gca tca cac gtt ttc ctt Phe Glu Gln Ile Gly Val Leu Ala Pro Ala Ala Ser His Val Phe Leu 100 105 110	515
tat atc aat gaa aaa aaa gaa ggc atc tat tta aaa atc gaa tct gtt Tyr Ile Asn Glu Lys Lys Glu Gly Ile Tyr Leu Lys Ile Glu Ser Val 115 120 125	563
gac gat cat ttc tta aag agg aga aat tta gaa agg ggg gcc att tat Asp Asp His Phe Leu Lys Arg Arg Asn Leu Glu Arg Gly Ala Ile Tyr 130 135 140	611
tat gcc gtt gat gac gat gct aat ttt tct ctg ctg agt tcc ttc aat Tyr Ala Val Asp Asp Asp Ala Asn Phe Ser Leu Leu Ser Ser Phe Asn 145 150 155	659
aaa aag gct aag caa aat ctc atg cag gga tac gaa aga aaa acg ggt Lys Lys Ala Lys Gln Asn Leu Met Gln Gly Tyr Glu Arg Lys Thr Gly 160 165 170 175	707
tca agc cgc cac gat gac tac ctc cat gag ttt atc tac ttt atc aat Ser Ser Arg His Asp Asp Tyr Leu His Glu Phe Ile Tyr Phe Ile Asn 180 185 190	755
acc gcc aaa gac gac ata ttt gaa aaa gaa atc aaa cgc tat ctc gat Thr Ala Lys Asp Asp Ile Phe Glu Lys Glu Ile Lys Arg Tyr Leu Asp 195 200 205	803
gtc aaa caa tat ttg ctg tgg ctc atc ggc gcc gtc tgc acc caa aat Val Lys Gln Tyr Leu Leu Trp Leu Ile Gly Ala Val Cys Thr Gln Asn 210 215 220	851
ttc gac ggc ttt gtc cat aat tac gcg ctt tat tta aac ggt cgc aca Phe Asp Gly Phe Val His Asn Tyr Ala Leu Tyr Leu Asn Gly Arg Thr 225 230 235	899
aaa acg ttt caa atc att cca tgg gat tat gac gcg aca tgg gga cgg Lys Thr Phe Gln Ile Ile Pro Trp Asp Tyr Asp Ala Thr Trp Gly Arg 240 245 250 255	947
aat att cac ggg gaa gaa atg gag cac aac cgg att ccg gcg aaa ggc Asn Ile His Gly Glu Glu Met Glu His Asn Arg Ile Pro Ala Lys Gly 260 265 270	995
tat aat acg ctg tct gca agg ctg ctc gac atc ccg gct ttt caa tcc Tyr Asn Thr Leu Ser Ala Arg Leu Leu Asp Ile Pro Ala Phe Gln Ser 275 280 285	1043
caa tac ttt aat tta atg aaa aat gtc ttg cac cgc caa ttt aca atc	1091

Gln Tyr Phe Asn Leu Met Lys Asn Val Leu His Arg Gln Phe Thr Ile	
290 295 300	
agc cgg ctt tcg cgg tat gcg gta aac tgg cac gag aca atc gcg cct	1139
Ser Arg Leu Ser Arg Tyr Ala Val Asn Trp His Glu Thr Ile Ala Pro	
305 310 315	
ttt ctt gaa cat gat cct tat aca acc gtc aca tac agc cgg ctc gaa	1187
Phe Leu Glu His Asp Pro Tyr Thr Thr Val Thr Tyr Ser Arg Leu Glu	
320 325 330 335	
gat gag caa aaa caa att ttt cat ttc atc gat cag agg aag cgg ttc	1235
Asp Glu Gln Lys Gln Ile Phe His Phe Ile Asp Gln Arg Lys Arg Phe	
340 345 350	
ctg ctt ttc gag ctt tcc cga taatagactg tcgctgtcct ccgaaaaaaaa	1286
Leu Leu Phe Glu Leu Ser Arg	
355	
tgtcacatttt tttgtcatat tggcgaaaaa aatccctttt acacaaaata aggtatacta	1346
gcaatatcaa ggacatcaat gcgctgaata cctgaaatta ccgactcaaa atacaaatcg	1406
aaagttggag actgccatga tgaacaataa aattgaagca aaaagactgg ccttatttga	1466
agctgccgaa aagttcggca tcaactccaa agaggccatt cgatgcagtc aggaattgga	1526
caacttgctg aatcaaagaa tgcaaaagga tgataactgc gtgcatgcgg aagaaagaaa	1586
aggccgccac acgtcatgac ctccgactgc aagctgcgcc tgatgccggc ctccttcctc	1646
ctccatttca tcatccgttg atttcgggtc gcagcttggg ctattcggcc attgtttttt	1706
gaacataaat catcgtgcaa ataccgtagg caagaatggc tgaagg	1752

<210> 12

<211> 358

<212> PRT

<213> Bacillus licheniformis

<400> 12

Met Met Ser Ala Thr Ala Leu Pro Ala Phe Arg Leu His Ile His Pro
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Lys His Leu Leu Glu Leu Lys Lys Asp Val Trp Ser Asp Glu Ala Val
20 25 30

Pro Gly Met Leu Leu Thr Gly Ser Ala Lys Thr Pro Val Ala Val Ser
35 40 45

Tyr Arg Gly Ala His Thr Arg Lys Leu Thr Lys Lys Ser Tyr Phe Ile
50 55 60

Gln Tyr Pro Asp Asn Lys Glu Lys Ala Ala Phe His Leu Asn Ala Glu  
65 70 75 80

Tyr His Asp Pro Ser Phe Ile Arg Asn Arg Leu Ser Phe His Phe Phe  
85 90 95

Glu Gln Ile Gly Val Leu Ala Pro Ala Ala Ser His Val Phe Leu Tyr  
100 105 110

Ile Asn Glu Lys Lys Glu Gly Ile Tyr Leu Lys Ile Glu Ser Val Asp  
115 120 125

Asp His Phe Leu Lys Arg Arg Asn Leu Glu Arg Gly Ala Ile Tyr Tyr  
130 135 140

Ala Val Asp Asp Asp Ala Asn Phe Ser Leu Leu Ser Ser Phe Asn Lys  
145 150 155 160

Lys Ala Lys Gln Asn Leu Met Gln Gly Tyr Glu Arg Lys Thr Gly Ser  
165 170 175

Ser Arg His Asp Asp Tyr Leu His Glu Phe Ile Tyr Phe Ile Asn Thr  
180 185 190

Ala Lys Asp Asp Ile Phe Glu Lys Glu Ile Lys Arg Tyr Leu Asp Val  
195 200 205

Lys Gln Tyr Leu Leu Trp Leu Ile Gly Ala Val Cys Thr Gln Asn Phe  
210 215 220

Asp Gly Phe Val His Asn Tyr Ala Leu Tyr Leu Asn Gly Arg Thr Lys  
225 230 235 240

Thr Phe Gln Ile Ile Pro Trp Asp Tyr Asp Ala Thr Trp Gly Arg Asn  
245 250 255

Ile His Gly Glu Glu Met Glu His Asn Arg Ile Pro Ala Lys Gly Tyr  
260 265 270

Asn Thr Leu Ser Ala Arg Leu Leu Asp Ile Pro Ala Phe Gln Ser Gln  
275 280 285

Tyr Phe Asn Leu Met Lys Asn Val Leu His Arg Gln Phe Thr Ile Ser  
 290 295 300

Arg Leu Ser Arg Tyr Ala Val Asn Trp His Glu Thr Ile Ala Pro Phe  
 305 310 315 320

Leu Glu His Asp Pro Tyr Thr Thr Val Thr Tyr Ser Arg Leu Glu Asp  
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Glu Gln Lys Gln Ile Phe His Phe Ile Asp Gln Arg Lys Arg Phe Leu  
 340 345 350

Leu Phe Glu Leu Ser Arg  
 355

<210> 13  
 <211> 1570  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1067)

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 cagttttccc cgatggaggc gctgcaaaaa gggacgcttt ggcccgtatt ttacgatcat 180  
 tatgaaaatc cgtatgaaga tgggaggtta ggagggtgac gaactcttta ccgcaagact 240  
 attataaaaag gcttcatgaa attcaggctg ttgattttgt catcgttgag ctgatgctat 300  
 accttgacac acatcccgat gataccgatg ccatcaaaca atacaaccag tatgccggat 360  
 tttccagaaa actgaaagcg aagtttgaat caaaatacgg ccctttgatt caaggaagcc 420  
 cggatcagac ggaatcctat tggagctgga aaagaagtcc ttggccatgg caagtttaat 480  
 agaggaaggg agtcaggttc atg tgg ctt tat gag aaa aaa ctg cag tat cct 533  
 Met Trp Leu Tyr Glu Lys Lys Leu Gln Tyr Pro  
 1 5 10  
 gtt agg gtg aga gaa tgc aat ccg aga ctt gcc aaa ttt ttg att gag 581  
 Val Arg Val Arg Glu Cys Asn Pro Arg Leu Ala Lys Phe Leu Ile Glu  
 15 20 25  
 caa tac ggc gga gcg gac ggc gaa ttg gct gcg gcg ctt cgc tat ttg 629

Gln Tyr Gly Gly Ala Asp Gly Glu Leu Ala Ala Ala Leu Arg Tyr Leu	
30 35 40	
aac cag cgc tac agc ata ccc gat aaa gtc gtc gga ctg ctg acg gac	677
Asn Gln Arg Tyr Ser Ile Pro Asp Lys Val Val Gly Leu Leu Thr Asp	
45 50 55	
atc ggt acg gaa gag ttt gct cac ctt gaa atg att gcc acg atg gta	725
Ile Gly Thr Glu Glu Phe Ala His Leu Glu Met Ile Ala Thr Met Val	
60 65 70 75	
tat aaa tta aca aaa gac gcg acg ccc gag cag atg aag gaa gcc ggg	773
Tyr Lys Leu Thr Lys Asp Ala Thr Pro Glu Gln Met Lys Glu Ala Gly	
80 85 90	
ctc ggc gat cat tac gca gac cat gac aaa gcc ctg ttt tat cat aac	821
Leu Gly Asp His Tyr Ala Asp His Asp Lys Ala Leu Phe Tyr His Asn	
95 100 105	
gct gcc ggc gtt ccg ttc acc gct aca tac atc cag gca aaa ggc gat	869
Ala Ala Gly Val Pro Phe Thr Ala Thr Tyr Ile Gln Ala Lys Gly Asp	
110 115 120	
ccg att gcc gat tta tat gaa gat ata gcg gct gaa gaa aaa gcg agg	917
Pro Ile Ala Asp Leu Tyr Glu Asp Ile Ala Ala Glu Glu Lys Ala Arg	
125 130 135	
gct acg tat caa tgg ctg att gac atg tcg gat gat ccg gat tta aat	965
Ala Thr Tyr Gln Trp Leu Ile Asp Met Ser Asp Asp Pro Asp Leu Asn	
140 145 150 155	
gac ggg ctg gcg ttt tta cgg gaa agg gaa atc gtt cat tca cag cgc	1013
Asp Gly Leu Ala Phe Leu Arg Glu Arg Glu Ile Val His Ser Gln Arg	
160 165 170	
ttc cgc gaa gct gtc gaa att ttg aag gaa gag cgc gac cgt aaa aaa	1061
Phe Arg Glu Ala Val Glu Ile Leu Lys Glu Glu Arg Asp Arg Lys Lys	
175 180 185	
gtg ttt taaacagcaa aaagccgaaa atacgaccgt attttcggct ttttatttac	1117
Val Phe	
tgcaccgggc tcgcaagcag ttctgctgcg cggtcgcgca gcacatatatt ttgaactttt	1177
ccggatgcgg tcagcgggta ttctgctgac agaaatacgt actccggaat ttataatac	1237
gaaagctgtc ctttgcaaaa atctctgacg tcttcgagcg tcagcttttt gcccggcctg	1297
catttaataa aggcagccgt tttttccccg tactttttcat ccggaacgcc gacaacctgt	1357
acatcgacaa tatcctcatg ttcataaagg aattcctcta tttcacgcgg gtaaatgttt	1417
tccccgccgc ggacgatcat atcttttaag cgccccggtaa tcctcacgta tccgtccccg	1477
tccattttctg ccaaattctcc ggtatggagc cagccgtctt catcgatggc cttttttgtg	1537



gcttcatcca ttttatagta gcctttcatg acg

1570

<210> 14

<211> 189

<212> PRT

<213> Bacillus licheniformis

<400> 14

Met Trp Leu Tyr Glu Lys Lys Leu Gln Tyr Pro Val Arg Val Arg Glu  
1 5 10 15

Cys Asn Pro Arg Leu Ala Lys Phe Leu Ile Glu Gln Tyr Gly Gly Ala  
20 25 30

Asp Gly Glu Leu Ala Ala Ala Leu Arg Tyr Leu Asn Gln Arg Tyr Ser  
35 40 45

Ile Pro Asp Lys Val Val Gly Leu Leu Thr Asp Ile Gly Thr Glu Glu  
50 55 60

Phe Ala His Leu Glu Met Ile Ala Thr Met Val Tyr Lys Leu Thr Lys  
65 70 75 80

Asp Ala Thr Pro Glu Gln Met Lys Glu Ala Gly Leu Gly Asp His Tyr  
85 90 95

Ala Asp His Asp Lys Ala Leu Phe Tyr His Asn Ala Ala Gly Val Pro  
100 105 110

Phe Thr Ala Thr Tyr Ile Gln Ala Lys Gly Asp Pro Ile Ala Asp Leu  
115 120 125

Tyr Glu Asp Ile Ala Ala Glu Glu Lys Ala Arg Ala Thr Tyr Gln Trp  
130 135 140

Leu Ile Asp Met Ser Asp Asp Pro Asp Leu Asn Asp Gly Leu Ala Phe  
145 150 155 160

Leu Arg Glu Arg Glu Ile Val His Ser Gln Arg Phe Arg Glu Ala Val  
165 170 175

Glu Ile Leu Lys Glu Glu Arg Asp Arg Lys Lys Val Phe  
180 185

<210> 15  
 <211> 1241  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (519)..(1028)

<400> 15  
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 aaatcggggga gtaaccagcg ataaagtctg gacgctctca gaagaagaaa aagaaaaatat 180  
 tttcaatatg ctggaagatc taaaaaaaca aaccgatgct ttggttcaaaa aacagaaaaga 240  
 aaaagcagcc gcaccgaatg aaaaaggggac aaagagagaa aagaacgctg atgcgtcatc 300  
 agaaaatggc gagagaccaa gaagaagaag aaacagaaca aatagactga gagaaaaact 360  
 tcgacaacgg agggagcaag aaaacacagc aacagcggaa aattcaaccg agtcagatac 420  
 ttcagcagaa aaaaatgggg atttgtagta gggatatctgt cttatacaag ttaaggagtt 480  
 acaacattta ataatagtaa atggaaggag gaaaagaa atg gaa aca aga cca tat 536  
 Met Glu Thr Arg Pro Tyr  
 1 5  
 tca tgg att gcg ctt gac ccg gaa tgc gaa cat cca ggc aac gat tat 584  
 Ser Trp Ile Ala Leu Asp Pro Glu Cys Glu His Pro Gly Asn Asp Tyr  
 10 15 20  
 cac cct agt tat cct aag aaa aaa tta tgt gac gac tat act tgc aac 632  
 His Pro Ser Tyr Pro Lys Lys Lys Leu Cys Asp Asp Tyr Thr Cys Asn  
 25 30 35  
 tgt ggt agg aaa ggg caa aat ggc ttt atc gat tct gac cta gat caa 680  
 Cys Gly Arg Lys Gly Gln Asn Gly Phe Ile Asp Ser Asp Leu Asp Gln  
 40 45 50  
 ctt cat ctt aac aaa cag ctc tca gat gaa acg atc atc att aaa gac 728  
 Leu His Leu Asn Lys Gln Leu Ser Asp Glu Thr Ile Ile Ile Lys Asp  
 55 60 65 70  
 tct tgt gat gtt caa gtc tca act gaa gac aca caa acg ttg gca tca 776  
 Ser Cys Asp Val Gln Val Ser Thr Glu Asp Thr Gln Thr Leu Ala Ser  
 75 80 85  
 gtc atg aca gct gca caa aca cta gct gtt act att att ctc gcc att 824  
 Val Met Thr Ala Ala Gln Thr Leu Ala Val Thr Ile Ile Leu Ala Ile  
 90 95 100  
 atc gat gat cct gat cta gcc gaa ctt gtc aca act gat ctg ttg cag 872

Ile Asp Asp Pro Asp Leu Ala Glu Leu Val Thr Thr Asp Leu Leu Gln  
105 110 115

gta act gcc aat aaa caa acg aac aga caa aaa ttg gtg atc gat aat 920  
Val Thr Ala Asn Lys Gln Thr Asn Arg Gln Lys Leu Val Ile Asp Asn  
120 125 130

tcc aga aat gta cat gtc aca acc gaa gat aca gac aca gct atc atc 968  
Ser Arg Asn Val His Val Thr Thr Glu Asp Thr Asp Thr Ala Ile Ile  
135 140 145 150

gta agc aca ttt gtt caa act gtt gta atc acc atc acc gcc ctt atc 1016  
Val Ser Thr Phe Val Gln Thr Val Val Ile Thr Ile Thr Ala Leu Ile  
155 160 165

gtc ggc ctt cta taattcaaaa agcagagcca accagctctg cttttcttca 1068  
Val Gly Leu Leu  
170

tttttataga cgattaccca caccaacaag ggcacgggta catatgttgt taaagactaa 1128

agtcaaatat ccctataaaa aggagctgaa atccatgagc tgcggaaaac accatggccg 1188

gcatgaaaat tgtgtatgcg atgcagtaga acagattata aaagaacagg atg 1241

<210> 16  
<211> 170  
<212> PRT  
<213> Bacillus licheniformis

<400> 16

Met Glu Thr Arg Pro Tyr Ser Trp Ile Ala Leu Asp Pro Glu Cys Glu  
1 5 10 15

His Pro Gly Asn Asp Tyr His Pro Ser Tyr Pro Lys Lys Lys Leu Cys  
20 25 30

Asp Asp Tyr Thr Cys Asn Cys Gly Arg Lys Gly Gln Asn Gly Phe Ile  
35 40 45

Asp Ser Asp Leu Asp Gln Leu His Leu Asn Lys Gln Leu Ser Asp Glu  
50 55 60

Thr Ile Ile Ile Lys Asp Ser Cys Asp Val Gln Val Ser Thr Glu Asp  
65 70 75 80

Thr Gln Thr Leu Ala Ser Val Met Thr Ala Ala Gln Thr Leu Ala Val  
85 90 95

Thr Ile Ile Leu Ala Ile Ile Asp Asp Pro Asp Leu Ala Glu Leu Val  
100 105 110

Thr Thr Asp Leu Leu Gln Val Thr Ala Asn Lys Gln Thr Asn Arg Gln  
115 120 125

Lys Leu Val Ile Asp Asn Ser Arg Asn Val His Val Thr Thr Glu Asp  
130 135 140

Thr Asp Thr Ala Ile Ile Val Ser Thr Phe Val Gln Thr Val Val Ile  
145 150 155 160

Thr Ile Thr Ala Leu Ile Val Gly Leu Leu  
165 170

<210> 17  
<211> 1516  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(1013)

<400> 17  
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tgggagctcc gtacggtatg gggggatacg gacagcagcc tgcaggggga cagatgttta 180  
acagaccgga agatgatgaa gactgattcg gaatgggacg atgatctatc gttccttttt 240  
tattgtggac cgctataaac attttcatgc tatttaacgg gaatgtctat aactgtcaag 300  
ggtaactctt cgcatcccg c acatcctaaa aaagagcgca atgctcaa at tcagcggttt 360  
tcacgggggg tactaccatt ggacagcaag ctgaaagtgt tttcggggat tttgcttttg 420  
acagcaggtc tatctgcatg cggaacgaac gacgctatag ataatggaaa caatacgcgc 480  
ccgatcggat attatctcaa atg atg cag atc gta atg cag ggt ctt gat aat 533  
Met Met Gln Ile Val Met Gln Gly Leu Asp Asn  
1 5 10  
gac ggc cct gtt aca gaa atg ctt gaa aac atg aac ggg aga cac ggt 581  
Asp Gly Pro Val Thr Glu Met Leu Glu Asn Met Asn Gly Arg His Gly  
15 20 25  
gca aca aac gta aac aat cga gcg gga aac ggc aat ccc gtt cca aca 629  
Ala Thr Asn Val Asn Asn Arg Ala Gly Asn Gly Asn Pro Val Pro Thr

30	35	40	
ggc gat gga act tac agc cgg gga gac atg aat tat cac aac cat ttg			677
Gly Asp Gly Thr Tyr Ser Arg Gly Asp Met Asn Tyr His Asn His Leu			
45	50	55	
gtg aat acg gcg gat aca ggc tat gac aga ccg gaa aac cgt aaa atc			725
Val Asn Thr Ala Asp Thr Gly Tyr Asp Arg Pro Glu Asn Arg Lys Ile			
60	65	70	75
tca agg aat atc act ggg cgc gtc aac aaa ttg aat tat gtt gac gaa			773
Ser Arg Asn Ile Thr Gly Arg Val Asn Lys Leu Asn Tyr Val Asp Glu			
	80	85	90
agc cag gca gtc gta acg aat gaa acg gtc atc atc gcc gta cgg tct			821
Ser Gln Ala Val Val Thr Asn Glu Thr Val Ile Ile Ala Val Arg Ser			
	95	100	105
gat aaa agg ctg aca aat aac gag aga act caa att aga aaa gca gcc			869
Asp Lys Arg Leu Thr Asn Asn Glu Arg Thr Gln Ile Arg Lys Ala Ala			
	110	115	120
aaa aca ttt gcc gga gac cgg acc gtt caa gtt gtc gag gac gac ggc			917
Lys Thr Phe Ala Gly Asp Arg Thr Val Gln Val Val Glu Asp Asp Gly			
	125	130	135
gca ttt aca agg ctg cgc gaa atg aac gat gat cct cag aac att agg			965
Ala Phe Thr Arg Leu Arg Glu Met Asn Asp Asp Pro Gln Asn Ile Arg			
140	145	150	155
gat cgc gga gac acg acg aat aac aat ttg aac cgc ttg cgg aac caa			1013
Asp Arg Gly Asp Thr Thr Asn Asn Asn Leu Asn Arg Leu Arg Asn Gln			
	160	165	170
taacaagcag ggaattgccg gggattcccc ggcaattttt tataagcgct cggccgattc			1073
ctttacaaaa acgggggaaaa ccgtataaag tgtacataga gacgagaatt attttggagg			1133
tagaaagtta tggctggcca ttctaaatgg aaaaatattc agagacgaaa aaatgcccaa			1193
gatgctaaac gcggcaaaat tttcatgaag cttgccaaag aaatatatgt agccgcgaaa			1253
gaaggggggac cagatccccga atctaacgca agtctgcgtc tcgtcatcga taaagccaaa			1313
aatgcaaaca tgccaaatga caacatcgac cgcgccatca aaaaagcttc cggcagccag			1373
gatggaaaaa gctatgagga aattacgtat gagggctacg gaccaagcgg tgtggctgtc			1433
atgggtcaaat gtttgacaga taataaaaac cggacggcga caagcgtcag aaccgctttc			1493
agcaaaaacg gcggcagctt ggg			1516

<210> 18  
 <211> 171  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 18

Met Met Gln Ile Val Met Gln Gly Leu Asp Asn Asp Gly Pro Val Thr  
1 5 10 15

Glu Met Leu Glu Asn Met Asn Gly Arg His Gly Ala Thr Asn Val Asn  
20 25 30

Asn Arg Ala Gly Asn Gly Asn Pro Val Pro Thr Gly Asp Gly Thr Tyr  
35 40 45

Ser Arg Gly Asp Met Asn Tyr His Asn His Leu Val Asn Thr Ala Asp  
50 55 60

Thr Gly Tyr Asp Arg Pro Glu Asn Arg Lys Ile Ser Arg Asn Ile Thr  
65 70 75 80

Gly Arg Val Asn Lys Leu Asn Tyr Val Asp Glu Ser Gln Ala Val Val  
85 90 95

Thr Asn Glu Thr Val Ile Ile Ala Val Arg Ser Asp Lys Arg Leu Thr  
100 105 110

Asn Asn Glu Arg Thr Gln Ile Arg Lys Ala Ala Lys Thr Phe Ala Gly  
115 120 125

Asp Arg Thr Val Gln Val Val Glu Asp Asp Gly Ala Phe Thr Arg Leu  
130 135 140

Arg Glu Met Asn Asp Asp Pro Gln Asn Ile Arg Asp Arg Gly Asp Thr  
145 150 155 160

Thr Asn Asn Asn Leu Asn Arg Leu Arg Asn Gln  
165 170

<210> 19

<211> 1249

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(746)

<400> 19  
catccttttta caagtgccgc tcacccgttt atttgagagg tataaatcct taacaacaat 60  
atcaattgga accgtttttt gcatttttggg gaatatcggg ttttctatcg caaatggctg 120  
gattgttttt atgcttttcca tgtttgttct gacaatcggc gaaattttat gttttccttc 180  
aatgaatgtc cttttggacg agctggctcc ggatcatatg aagggcgcggt attacggcat 240  
gcaaaaactta tacaacatcg gtgagttttt agggccttgg ctgggggggaa tgatgcttgc 300  
cttgtagcggg ggaaaagccg tctttcttat tgctgcgtgt tcagtctttt tggcttttagg 360  
cgcttaccat gtgggaagga gaaagttttt atctgcacag cattatgggtg tatcgccttt 420  
ttcttattga aaatttaggc cgcttatgca tgaatcatta agaattaccc aacctaaaag 480  
gtaaaaaagg agtatgaatc atg gac aca aca ttg ggc tac ctc cgt gag tca 533  
Met Asp Thr Thr Leu Gly Tyr Leu Arg Glu Ser  
1 5 10  
ctg tcg aat cac ctt gaa cac ggc ata gga caa aac att tac aga aaa 581  
Leu Ser Asn His Leu Glu His Gly Ile Gly Gln Asn Ile Tyr Arg Lys  
15 20 25  
atc gtt tcc ggg cga tat gcc aat gag gaa gag ttt gtc gag cac ttg 629  
Ile Val Ser Gly Arg Tyr Ala Asn Glu Glu Glu Phe Val Glu His Leu  
30 35 40  
gag gag cgg gaa atg gaa ttt ctg aat caa gtg ctt gaa cat gag atg 677  
Glu Glu Arg Glu Met Glu Phe Leu Asn Gln Val Leu Glu His Glu Met  
45 50 55  
aaa tat gcg ctg aat gaa cag gac cat aaa cgg aca aga gaa tta aac 725  
Lys Tyr Ala Leu Asn Glu Gln Asp His Lys Arg Thr Arg Glu Leu Asn  
60 65 70 75  
gaa gtg tat gaa ctg ctg ttt tgaaaggcgg gaatgatcaa tgggtgcaat 776  
Glu Val Tyr Glu Leu Leu Phe  
80  
agagcggaac ggatacacgt ttgaaccgga atacagcgtg accagacaaa acggtgcgat 836  
ccatgtatac cggcgcggcc ggtttgtcga ggagattccc tttgagtttc acggggagtt 896  
tccagagcat gatttaattg aagagcttgt caatcattat tgttatgaaa ataaaatata 956  
aggcttgaag aggctgccga ccgggcggct tttatttttg gatttttata tctataatcc 1016  
gcttgagttt ttttagaacg gcagcagaaa agctgccata aatatgacag ctcatgcatc 1076  
gctatttttt cttttcgtcg tagtattgaa cagggtacat ggatccttcc gataaccattt 1136  
tgttatcttc gatatcatgc ggagacgggt gtctgtcttt ttcaaccggg aatgaatcta 1196  
cgttgtgttt ttccgaaaag taagggatct tttctttgac gttttgcaag tac 1249

<210> 20  
 <211> 82  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 20

Met Asp Thr Thr Leu Gly Tyr Leu Arg Glu Ser Leu Ser Asn His Leu  
 1 5 10 15

Glu His Gly Ile Gly Gln Asn Ile Tyr Arg Lys Ile Val Ser Gly Arg  
 20 25 30

Tyr Ala Asn Glu Glu Glu Phe Val Glu His Leu Glu Glu Arg Glu Met  
 35 40 45

Glu Phe Leu Asn Gln Val Leu Glu His Glu Met Lys Tyr Ala Leu Asn  
 50 55 60

Glu Gln Asp His Lys Arg Thr Arg Glu Leu Asn Glu Val Tyr Glu Leu  
 65 70 75 80

Leu Phe

<210> 21  
 <211> 1620  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1121)

<400> 21

cttcgtgaaa aatacagttc taaagatcaa aaaacgcagc agaagcttca acaggaaaacg 60  
 atggctctca tgcagaagca cggggttaac ccgcttgccg gatgtttccc gatcttaatt 120  
 caaatgccga ttttaatcgg attctatcat gccattatga gaacgcggga aatcgcagaa 180  
 cacagctttt tatggtttga ccttggggag cgtgatccgt atttcatttt gccgattctc 240  
 gccggtgtgt tcacattcat tcagcaaaag ctgatgatgg cgggaacagc gcagcaaaat 300  
 ccgcagatgg cgatgatgct ttggctgatg ccgatcatga tcgttgattt tgcgatcagt 360  
 ttcccggcgg ctctttccct gtactgggta gtcggtaact tattcatgat tgctcaaacc 420



ttctttatca aagggcctga tctaaaggct gagagacagg aagcggcagc cggaggaaaa	480
aaatccggag gtaagaaaaa gtg aag gaa ctg act gct act gga cgt acc gtc	533
Val Lys Glu Leu Thr Ala Thr Gly Arg Thr Val	
1 5 10	
gat gaa gca gtg caa tcc ggg ctt gaa cag ctg ggc ctt cat gca gat	581
Asp Glu Ala Val Gln Ser Gly Leu Glu Gln Leu Gly Leu His Ala Asp	
15 20 25	
gat gtc gaa gtc gac gta gtt gat gaa gga aaa aag gga tta ttc ggc	629
Asp Val Glu Val Asp Val Val Asp Glu Gly Lys Lys Gly Leu Phe Gly	
30 35 40	
att ttc ggt cat cgg tct gca gtc gtg aac att cgg gaa aaa ata gac	677
Ile Phe Gly His Arg Ser Ala Val Val Asn Ile Arg Glu Lys Ile Asp	
45 50 55	
ccg gtt aaa gaa gca aaa caa tat ttg gaa aat gta att tcg aat atg	725
Pro Val Lys Glu Ala Lys Gln Tyr Leu Glu Asn Val Ile Ser Asn Met	
60 65 70 75	
gga ata caa gcc cag gtg acg gca gaa gag gag tct aaa cga gtg gtt	773
Gly Ile Gln Ala Gln Val Thr Ala Glu Glu Glu Ser Lys Arg Val Val	
80 85 90	
ttt cag ttg aaa gga gac aaa aca gct ctt tta att gga aaa agg gga	821
Phe Gln Leu Lys Gly Asp Lys Thr Ala Leu Leu Ile Gly Lys Arg Gly	
95 100 105	
caa act tta aat gcc ctt gaa acg ctg acg cag ctc gtg ctc aat cgt	869
Gln Thr Leu Asn Ala Leu Glu Thr Leu Thr Gln Leu Val Leu Asn Arg	
110 115 120	
cat tcc gac aga tat atc caa gcg gtg gtt gac gcc gaa gga tac cgc	917
His Ser Asp Arg Tyr Ile Gln Ala Val Val Asp Ala Glu Gly Tyr Arg	
125 130 135	
gca aag cgg aag gaa aca ctt gct cag ctg gca ttg aag ctt gct gac	965
Ala Lys Arg Lys Glu Thr Leu Ala Gln Leu Ala Leu Lys Leu Ala Asp	
140 145 150 155	
cag gcg gcc agg cag aaa aaa gac att cac ctg gag ccg atg cct tcc	1013
Gln Ala Ala Arg Gln Lys Lys Asp Ile His Leu Glu Pro Met Pro Ser	
160 165 170	
agt gag cgc aag gtc atc cat gat acg ctt gcg ggc tac tcg cag cat	1061
Ser Glu Arg Lys Val Ile His Asp Thr Leu Ala Gly Tyr Ser Gln His	
175 180 185	
atc gaa act tac tct acc ggt gaa gac cat aac cgg cac ctt gtc atc	1109
Ile Glu Thr Tyr Ser Thr Gly Glu Asp His Asn Arg His Leu Val Ile	
190 195 200	
tca tat aaa aaa taacatgaaa accgaagttc ccaaaattgg ggcttcggtt	1161
Ser Tyr Lys Lys	
205	

tttttgccgt tgaaaatcga tgaaatgcag caaaatcagt ttaagttcta ttttttcagg 1221  
 cgtaagctgt tgatgaaaat gaaatttaat tgttattcac atgtggataa gttaaagtaa 1281  
 gtaatgatgg cttagaacgg ttgtggataa cggttcaagt cacttccact tcaattgaaa 1341  
 ctatgttatc tttaaatttt gattacaata aaagtttttc atccgtatac gatgtttgga 1401  
 agatgacccg gcaaatgggg ataatagata taggaatgaa aaagagaggt gaaagccatg 1461  
 gataccatcg ctgcgatttc aacgccgatg ggagaagggg cgattgcgat cgtccggatg 1521  
 agcggccctg aggctcttgc gatcgccgat aaagtgtata aaggacctcg cggaaaaagg 1581  
 ctgagttccg tcgattcaca tacgattaac tacgggtcat 1620

<210> 22  
 <211> 207  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 22

Val Lys Glu Leu Thr Ala Thr Gly Arg Thr Val Asp Glu Ala Val Gln  
 1 5 10 15

Ser Gly Leu Glu Gln Leu Gly Leu His Ala Asp Asp Val Glu Val Asp  
 20 25 30

Val Val Asp Glu Gly Lys Lys Gly Leu Phe Gly Ile Phe Gly His Arg  
 35 40 45

Ser Ala Val Val Asn Ile Arg Glu Lys Ile Asp Pro Val Lys Glu Ala  
 50 55 60

Lys Gln Tyr Leu Glu Asn Val Ile Ser Asn Met Gly Ile Gln Ala Gln  
 65 70 75 80

Val Thr Ala Glu Glu Glu Ser Lys Arg Val Val Phe Gln Leu Lys Gly  
 85 90 95

Asp Lys Thr Ala Leu Leu Ile Gly Lys Arg Gly Gln Thr Leu Asn Ala  
 100 105 110

Leu Glu Thr Leu Thr Gln Leu Val Leu Asn Arg His Ser Asp Arg Tyr  
 115 120 125

Ile Gln Ala Val Val Asp Ala Glu Gly Tyr Arg Ala Lys Arg Lys Glu  
 130 135 140

Thr Leu Ala Gln Leu Ala Leu Lys Leu Ala Asp Gln Ala Ala Arg Gln  
 145 150 155 160

Lys Lys Asp Ile His Leu Glu Pro Met Pro Ser Ser Glu Arg Lys Val  
 165 170 175

Ile His Asp Thr Leu Ala Gly Tyr Ser Gln His Ile Glu Thr Tyr Ser  
 180 185 190

Thr Gly Glu Asp His Asn Arg His Leu Val Ile Ser Tyr Lys Lys  
 195 200 205

<210> 23  
 <211> 1614  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1115)

<400> 23  
 gtgtttatcg ccgaaccttc cccaaaaagg agaaactaaa aaggccatca aaaatgtgac 60  
 gccgaaaacg tatccgctcc attttgcctg aaatccgtcc gaatagctgc caagcgtctc 120  
 aatatagagg gaaagaaacg gcagaacatc tgtggagctt gcggccacga aaaaattcgc 180  
 aaaccacatg atcacaaggt ttttcttata aacagagatg cgaatcacct tcttaaaaaa 240  
 tttgaattcc ctttcattat aaatgaaatg cgaaagctgc atggaattga tgctctatag 300  
 aatgacgaaa aatgggcatt tgaaggaatt ttcaacattt tcagaaaata aaaccttaaa 360  
 tatagaaata taatgatata ataagagaaa tatgagcgta ctttggaata cattcagaag 420  
 actataggct tggataattt caatccgctg cgttaccacc ataagttttt tatattgaga 480  
 tagaaaggca ggtgtgaaag ttg gaa gcg agc acc tta ctg att att gat ttt 533  
 Leu Glu Ala Ser Thr Leu Leu Ile Ile Asp Phe  
 1 5 10  
 gaa ttt aca atg cct gag gga aag tat cac ccg caa aat ttt ttc ccg 581  
 Glu Phe Thr Met Pro Glu Gly Lys Tyr His Pro Gln Asn Phe Phe Pro  
 15 20 25  
 gaa atc ata gaa gca ggg att gta aag acg gtt cat gat gag gtg gtt 629  
 Glu Ile Ile Glu Ala Gly Ile Val Lys Thr Val His Asp Glu Val Val

30	35	40	
gag acg ttt tca agc tat att aag ccg aag aag ttc cct aaa tta acg			677
Glu Thr Phe Ser Ser Tyr Ile Lys Pro Lys Lys Phe Pro Lys Leu Thr			
45	50	55	
agg cgc tgc aaa aat ttt ctc agc atc acg cag gaa cag gtt gac caa			725
Arg Arg Cys Lys Asn Phe Leu Ser Ile Thr Gln Glu Gln Val Asp Gln			
60	65	70	75
ggc atc acg ttt aac gcg ctg att gaa aag ctg cgg gag ctt gat cct			773
Gly Ile Thr Phe Asn Ala Leu Ile Glu Lys Leu Arg Glu Leu Asp Pro			
	80	85	90
gac cga aac agc gtc atc att aca tgg gga aac atg gat atg aaa gtg			821
Asp Arg Asn Ser Val Ile Ile Thr Trp Gly Asn Met Asp Met Lys Val			
	95	100	105
ctg aag caa aat tgc atg ttc aac cat gtt ccg ttt ccg ttt aaa gga			869
Leu Lys Gln Asn Cys Met Phe Asn His Val Pro Phe Pro Phe Lys Gly			
	110	115	120
gag atg agg gac ctt tcc atg gag tac aag gaa ttt ttc ggc gac aaa			917
Glu Met Arg Asp Leu Ser Met Glu Tyr Lys Glu Phe Phe Gly Asp Lys			
	125	130	135
aca ttg acg aat ttg tgg aag gca gcg gaa gag tac ggc gat tca gga			965
Thr Leu Thr Asn Leu Trp Lys Ala Ala Glu Glu Tyr Gly Asp Ser Gly			
	140	145	150
acg gga aaa cag cat aaa gcg ctt gac gac gcg atg aca acg tat aag			1013
Thr Gly Lys Gln His Lys Ala Leu Asp Asp Ala Met Thr Thr Tyr Lys			
	160	165	170
ttg ttt cgg ctc gta gaa cgg gat aag aag tat ttg gaa aat ccg aag			1061
Leu Phe Arg Leu Val Glu Arg Asp Lys Lys Tyr Leu Glu Asn Pro Lys			
	175	180	185
ccg acg acg atc ggc gaa cgg gtt gac ctc tca aaa gtc ttt ccg cac			1109
Pro Thr Thr Ile Gly Glu Arg Val Asp Leu Ser Lys Val Phe Pro His			
	190	195	200
gcc aca taaaaaaccc aatctgacaa acagattggg ttatttgtgc aggaaatatt			1165
Ala Thr			
205			
ctttttcaag cccatgaata agctcaagcg attttgccgc gtattcggac gaatcgtttt			1225
gcagatccgt ttttaagcgg ctcaaagctg agcggagcga atccgcataa tccggtacag			1285
cttcatcgaa cggcttcacc atgcggtgcg ggatattcgt ctgttcaccg taagcgagcg			1345
cttttcgttc atgaaaaaaaaa gggacgtctg cccgattggg atgatgaagg tcgccctgct			1405
tcggatgggt cagcacggcg aggattttga ccaggtagtg catcggttta acatccgtaa			1465
tttcgccgat gtagacgcct gttttataaa agccctttac gcgatctccg acttgaaatt			1525

ggttgttcac tgcattctgcc tcctaattggt atcataataa ataaatggta aaaaaatcat 1585  
 ttcagggagg aagaaaaatg gcgccgttt 1614

<210> 24  
 <211> 205  
 <212> PRT  
 <213> Bacillus licheniformis  
 <400> 24

Leu Glu Ala Ser Thr Leu Leu Ile Ile Asp Phe Glu Phe Thr Met Pro  
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Glu Gly Lys Tyr His Pro Gln Asn Phe Phe Pro Glu Ile Ile Glu Ala  
 20 25 30

Gly Ile Val Lys Thr Val His Asp Glu Val Val Glu Thr Phe Ser Ser  
 35 40 45

Tyr Ile Lys Pro Lys Lys Phe Pro Lys Leu Thr Arg Arg Cys Lys Asn  
 50 55 60

Phe Leu Ser Ile Thr Gln Glu Gln Val Asp Gln Gly Ile Thr Phe Asn  
 65 70 75 80

Ala Leu Ile Glu Lys Leu Arg Glu Leu Asp Pro Asp Arg Asn Ser Val  
 85 90 95

Ile Ile Thr Trp Gly Asn Met Asp Met Lys Val Leu Lys Gln Asn Cys  
 100 105 110

Met Phe Asn His Val Pro Phe Pro Phe Lys Gly Glu Met Arg Asp Leu  
 115 120 125

Ser Met Glu Tyr Lys Glu Phe Phe Gly Asp Lys Thr Leu Thr Asn Leu  
 130 135 140

Trp Lys Ala Ala Glu Glu Tyr Gly Asp Ser Gly Thr Gly Lys Gln His  
 145 150 155 160

Lys Ala Leu Asp Asp Ala Met Thr Thr Tyr Lys Leu Phe Arg Leu Val  
 165 170 175

Glu Arg Asp Lys Lys Tyr Leu Glu Asn Pro Lys Pro Thr Thr Ile Gly  
180 185 190

Glu Arg Val Asp Leu Ser Lys Val Phe Pro His Ala Thr  
195 200 205

<210> 25  
<211> 1600  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(1097)

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ttccaaaatt cagctccttt tttggagggtc attgtttttt caacgggttc tttgacagtt 180  
ttttcatcca ttacaagtgt ttcatttaat ttgtcatcat ttaatatctt ttgaatcgct 240  
ttttttccgt catctgtctt taatatatcg acaaccattt ttttggtttg atcatagtcc 300  
atctcagctg cttggtccgt gggagcacaa gctgttacag atagaaacag aaaacagctt 360  
atcgatagca ttgcggtctt gaacatgctt aagctccttt cgaaaactcg tcttaccttt 420  
aatatgaatg tcttttaaaa atttatacat aacaaaatat cgctgtttaca gcggttttatt 480  
taggggttgg gaagtctaca atg aaa agc cgt aat ctc gtc cga ttt ttc ttt 533  
Met Lys Ser Arg Asn Leu Val Arg Phe Phe Phe  
1 5 10  
tcc gta ttg ggt gtc gga gct ttg act aca agt att gtc ggt ttt gcc 581  
Ser Val Leu Gly Val Gly Ala Leu Thr Thr Ser Ile Val Gly Phe Ala  
15 20 25  
ata gag tgg gga aga tat aag gag ctg ttt ctt tcc ttc gag gta ttg 629  
Ile Glu Trp Gly Arg Tyr Lys Glu Leu Phe Leu Ser Phe Glu Val Leu  
30 35 40  
gag att ctg tct gtt ctt ttc tgg ttt atc ggg gtt ggc atg atc ttt 677  
Glu Ile Leu Ser Val Leu Phe Trp Phe Ile Gly Val Gly Met Ile Phe  
45 50 55  
agc gtg att gct caa atg gga ttt gtg att ttc tta acg att cac cgc 725  
Ser Val Ile Ala Gln Met Gly Phe Val Ile Phe Leu Thr Ile His Arg  
60 65 70 75  
ttt gca ctg gaa att ttc aga tct cat tct ttg tgg aat tcg att cag 773  
Phe Ala Leu Glu Ile Phe Arg Ser His Ser Leu Trp Asn Ser Ile Gln

80	85	90	
ctg ttt ttg att ata ttt gtc gcg ttt gac ttg gtt tac ttg cgc ttt			821
Leu Phe Leu Ile Ile Phe Val Ala Phe Asp Leu Val Tyr Leu Arg Phe			
95	100	105	
ctg ttt ttt gaa aaa gat gga ggc tcc atc att ccg tac att tgg ctg			869
Leu Phe Phe Glu Lys Asp Gly Gly Ser Ile Ile Pro Tyr Ile Trp Leu			
110	115	120	
ccg ctc ttt att ttg gcg gta ggc att gcg gcc gct tat gca aag caa			917
Pro Leu Phe Ile Leu Ala Val Gly Ile Ala Ala Tyr Ala Lys Gln			
125	130	135	
aaa cag tcc tct aaa aaa acg ttc gtt tcc gca tta ttt cta atg ttt			965
Lys Gln Ser Ser Lys Lys Thr Phe Val Ser Ala Leu Phe Leu Met Phe			
140	145	150	155
gtt ttt act gtg atg gag tgg ttc ccg gcg tta agg gtc aat gaa gag			1013
Val Phe Thr Val Met Glu Trp Phe Pro Ala Leu Arg Val Asn Glu Glu			
160	165	170	
gac tgg ctc tat tta atg ctg ctt cct tta tta gcc tgc aac gct ttt			1061
Asp Trp Leu Tyr Leu Met Leu Leu Pro Leu Leu Ala Cys Asn Ala Phe			
175	180	185	
cag ctt tta atg ctg cca aaa ttt cag gca cgc gct tagaccggct			1107
Gln Leu Leu Met Leu Pro Lys Phe Gln Ala Arg Ala			
190	195		
gctacttttac ttctgaagat tttgcatccg tattttgcgat taattcgctg actgttacgt			1167
ttttgagccc cttgcttctg agatggtgca cgatctctgg cagggcttct tttgtttgtt			1227
tggcggaatc tgaagcgtga aagagcacga tgtcaccggc gtttaccgtt ccattttacgt			1287
tttggacgat cttttgaacc cccgggttcg tccagtcacg cgagttaata ctataatgaa			1347
caacggtgta gccgtactgt ttagcaacat cgagtacgtc tttattaaac tggccggtcg			1407
gcggtcttaa aagcgtgaagg tcgtcaagcc cgagtttttg aaaggagtgt cgtgcttttg			1467
ctaagtcttt tttgatctcg cttttcttca tttgcgaata gtttttataa gcatagccca			1527
tactcccgat ctggtgacca tctttacgga ttctttctac gacatccggg tggcgctctg			1587
cccatgaagc tga			1600

<210> 26

<211> 199

<212> PRT

<213> Bacillus licheniformis

<400> 26

Met Lys Ser Arg Asn Leu Val Arg Phe Phe Phe Ser Val Leu Gly Val

1	5	10	15
Gly	Ala	Leu	Thr
Thr	Ser	Ile	Val
Gly	Phe	Ala	Ile
Glu	Trp	Gly	Arg
20	25	30	
Tyr	Lys	Glu	Leu
Phe	Leu	Ser	Phe
Glu	Val	Leu	Glu
Ile	Leu	Ser	Val
35	40	45	
Leu	Phe	Trp	Phe
Ile	Gly	Val	Gly
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Val	Ile	Ala	Gln
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Met	Gly	Phe	Val
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Phe	Arg	Ser	His
Ser	Leu	Trp	Asn
Ser	Ile	Gln	Leu
Phe	Leu	Ile	Ile
85	90	95	
Phe	Val	Ala	Phe
Asp	Leu	Val	Tyr
Leu	Arg	Phe	Leu
Phe	Phe	Glu	Lys
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Asp	Gly	Gly	Ser
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Ile	Trp	Leu	Pro
Leu	Phe	Ile	Leu
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Ala	Ala	Ala	Tyr
Ala	Lys	Gln	Lys
Gln	Ser	Ser	Lys
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Lys	Thr	Phe	Val
Ser	Ala	Leu	Phe
Leu	Met	Phe	Val
Phe	Thr	Val	Met
145	150	155	160
Glu	Trp	Phe	Pro
Ala	Leu	Arg	Val
Asn	Glu	Glu	Asp
Trp	Leu	Tyr	Leu
165	170	175	
Met	Leu	Leu	Pro
Leu	Leu	Ala	Cys
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gaaaagatag ccgcaccgcg gcggtcatct cctcggactt cgattcccgc cggttcagtc	300
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Leu Ser Ile Glu Val Leu Lys Pro Gly Leu Met Thr Thr Val	
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caa gac ttg ggc cgc aca ggt ttt caa aaa tac ggc gtg ctt gtc agc	578
Gln Asp Leu Gly Arg Thr Gly Phe Gln Lys Tyr Gly Val Leu Val Ser	
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ggt gcc atg gat gcc gat tct ttg cgg att gcc aat ctg ctc gcg ggg	626
Gly Ala Met Asp Ala Asp Ser Leu Arg Ile Ala Asn Leu Leu Ala Gly	
35 40 45	
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Asn Ser Gln Asn Glu Ala Ala Leu Glu Val Thr Leu Met Gly Pro Gly	
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Pro Ser Leu Arg Phe Gln Lys Pro Ala Leu Ile Ala Val Thr Gly Ala	
65 70 75	
gac ttt tca ctg atg gta aat gac gaa gaa gtc ccg ctt tgg cgc ccg	770
Asp Phe Ser Leu Met Val Asn Asp Glu Glu Val Pro Leu Trp Arg Pro	
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gtt ttc atc aaa gag ggc agc gtg ttg aca ttc ggc atg tgc aag cgc	818
Val Phe Ile Lys Glu Gly Ser Val Leu Thr Phe Gly Met Cys Lys Arg	
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Gly Ser Arg Ala Tyr Met Ala Val Ala Gly Gly Ile Asp Val Pro Pro	
115 120 125	
gta atg gaa agc aaa agc aca tat gtc aga gca gga ctc ggc ggc ttt	914
Val Met Glu Ser Lys Ser Thr Tyr Val Arg Ala Gly Leu Gly Gly Phe	
130 135 140	

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gaa cgg ggc ttt gcg gct ccg aag tgg gct gtc gac cgc aaa tat ttt Glu Arg Gly Phe Ala Ala Pro Lys Trp Ala Val Asp Arg Lys Tyr Phe 175 180 185 190	1058
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ctc gca gac agg cag aca gcg ggc gga tac ccg aga atc gcc cat atc Leu Ala Asp Arg Gln Thr Ala Gly Gly Tyr Pro Arg Ile Ala His Ile 275 280 285	1346
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gaa cgg gag acg aaa atc agc gaa ctt tct gcc cga ttg aag ctt gaa Glu Arg Glu Thr Lys Ile Ser Glu Leu Ser Ala Arg Leu Lys Leu Glu 320 325 330	1490
tac atg tta tgataggtgt gatgtgtatc aggaggggga aggcatggaa Tyr Met Leu 335	1539
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Gln Asn Glu Ala Ala Leu Glu Val Thr Leu Met Gly Pro Gly Pro Ser  
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Ser Leu Met Val Asn Asp Glu Glu Val Pro Leu Trp Arg Pro Val Phe  
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Ile Lys Glu Gly Ser Val Leu Thr Phe Gly Met Cys Lys Arg Gly Ser  
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Arg Ala Tyr Met Ala Val Ala Gly Gly Ile Asp Val Pro Pro Val Met  
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 145 150 155 160

Leu Ser Glu Ala Leu His Arg Lys Leu Ala Asp Glu Gly Lys Glu Arg  
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Leu Lys Lys Asn Pro Val Ile Arg Val Ile Lys Gly Asp Gln Phe Ala  
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Cys Phe Thr Ser Ser Ser Gln Glu Arg Phe Phe Ala Gly Pro Phe Arg  
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Val Thr Ala Lys Ser Asp Arg Met Gly Tyr Arg Leu Gln Gly Glu Ala  
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Gly Thr Ile Gln Val Pro Pro Asp Gly Asn Pro Ile Val Leu Leu Ala  
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Asp Arg Gln Thr Ala Gly Gly Tyr Pro Arg Ile Ala His Ile Ala Ser  
275 280 285

Ala Asp Phe Ser Gln Val Thr Gln Met Met Pro Gly Glu Gln Val Gln  
290 295 300

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Leu

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ggc gga gac gga ggc aac ggt atg gtt gct ttc cgc cgc gaa aaa tat      581
Gly Gly Asp Gly Gly Asn Gly Met Val Ala Phe Arg Arg Glu Lys Tyr
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Val Pro Lys Gly Gly Pro Ala Gly Gly Asp Gly Gly Lys Gly Gly Asp
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Val Val Phe Lys Val Asp Glu Gly Leu Ser Thr Leu Met Asp Phe Arg
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tat caa aga cat ttt aag gca gcg cgc gga gaa cac ggc atg tct aaa      725
Tyr Gln Arg His Phe Lys Ala Ala Arg Gly Glu His Gly Met Ser Lys
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aac cag cac ggc cga aat gcc gaa gac atg gtt gtg aaa gtc ccg ccc      773
Asn Gln His Gly Arg Asn Ala Glu Asp Met Val Val Lys Val Pro Pro
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ggc acg gtt gtc att gac gat gat aca aaa cag gtc atc gct gat tta      821
Gly Thr Val Val Ile Asp Asp Asp Thr Lys Gln Val Ile Ala Asp Leu
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acg gag cac gga cag gaa gcc gtc atc gca aaa ggc gga cgc ggc gga      869
Thr Glu His Gly Gln Glu Ala Val Ile Ala Lys Gly Gly Arg Gly Gly
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cgg ggc aat aca cgt ttt gcg acg cct gcc aac ccg gcg ccg cag ctt      917
Arg Gly Asn Thr Arg Phe Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu
                        125          130          135

tct gaa aac ggc gaa ccc ggc aag gag cgc tat att gtt ctc gag ctg      965

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Lys	Val	Leu	Ala	Asp	Val	Gly	Leu	Val	Gly	Phe	Pro	Ser	Val	Gly	Lys		
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Ser	Thr	Leu	Leu	Ser	Val	Val	Ser	Ser	Ala	Lys	Pro	Lys	Ile	Ala	Asp		
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tac	cac	ttt	aca	acg	ctg	aac	ccg	aat	ctc	gga	atg	gtc	gaa	acg	gaa		1109
Tyr	His	Phe	Thr	Thr	Leu	Asn	Pro	Asn	Leu	Gly	Met	Val	Glu	Thr	Glu		
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gac	ggc	cgc	agc	ttt	gta	atg	gcg	gat	ctt	ccg	gga	ctg	att	gag	ggg		1157
Asp	Gly	Arg	Ser	Phe	Val	Met	Ala	Asp	Leu	Pro	Gly	Leu	Ile	Glu	Gly		
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Ala	His	Glu	Gly	Val	Gly	Leu	Gly	His	Gln	Phe	Leu	Arg	His	Ile	Glu		
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Arg	Thr	Arg	Val	Ile	Val	His	Val	Ile	Asp	Met	Ser	Gly	Leu	Glu	Gly		
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cgc	gac	ccg	tat	gaa	gat	tat	gtg	acc	att	aat	aaa	gag	ctt	gaa	cag		1301
Arg	Asp	Pro	Tyr	Glu	Asp	Tyr	Val	Thr	Ile	Asn	Lys	Glu	Leu	Glu	Gln		
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Tyr	Asn	Leu	Arg	Leu	Thr	Glu	Arg	Pro	Gln	Ile	Ile	Val	Ala	Asn	Lys		
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atg	gat	atg	ccg	gat	gcg	gaa	gaa	aat	ctg	aag	gct	ttc	aaa	gaa	aag		1397
Met	Asp	Met	Pro	Asp	Ala	Glu	Glu	Asn	Leu	Lys	Ala	Phe	Lys	Glu	Lys		
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Leu	Thr	Asp	Asp	Tyr	Pro	Val	Phe	Pro	Ile	Ser	Ala	Val	Thr	Arg	Gln		
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Gly	Leu	Arg	Asp	Leu	Leu	Phe	Glu	Ile	Ala	Asp	Arg	Leu	Glu	Thr	Thr		
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Pro	Glu	Phe	Pro	Leu	Tyr	Asp	Glu	Glu	Asp	Met	Ala	Glu	Asn	Arg	Val		
			335					340					345				
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Met	Tyr	Lys	Leu	Glu	Asp	Glu	Glu	Ala	Pro	Phe	Glu	Ile	Ser	Arg	Asp		
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cct	gac	ggc	acc	ttc	gtg	ctc	agc	gga	gcc	aag	ctt	gaa	cgc	tta	ttt		1637
Pro	Asp	Gly	Thr	Phe	Val	Leu	Ser	Gly	Ala	Lys	Leu	Glu	Arg	Leu	Phe		

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Lys Met Thr Asp Phe Ser Arg Asp Glu Ser Val Lys Arg Phe Ala Arg			
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cag ctt cgc gga atg ggc gtc gat gat gcg ctt cgg gcc cgc ggt gca			1733
Gln Leu Arg Gly Met Gly Val Asp Asp Ala Leu Arg Ala Arg Gly Ala			
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Lys Asp Gly Asp Thr Ile Arg Leu Leu Glu Phe Glu Phe Glu Phe Ile			
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Glu Ala Val Ile Ala Lys Gly Gly Arg Gly Gly Arg Gly Asn Thr Arg  
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Phe Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu Ser Glu Asn Gly Glu  
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Pro Gly Lys Glu Arg Tyr Ile Val Leu Glu Leu Lys Val Leu Ala Asp  
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Val Gly Leu Val Gly Phe Pro Ser Val Gly Lys Ser Thr Leu Leu Ser  
165 170 175

Val Val Ser Ser Ala Lys Pro Lys Ile Ala Asp Tyr His Phe Thr Thr  
180 185 190

Leu Asn Pro Asn Leu Gly Met Val Glu Thr Glu Asp Gly Arg Ser Phe  
195 200 205

Val Met Ala Asp Leu Pro Gly Leu Ile Glu Gly Ala His Glu Gly Val  
210 215 220

Gly Leu Gly His Gln Phe Leu Arg His Ile Glu Arg Thr Arg Val Ile  
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Leu Phe Glu Ile Ala Asp Arg Leu Glu Thr Thr Pro Glu Phe Pro Leu  
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Val Leu Ser Gly Ala Lys Leu Glu Arg Leu Phe Lys Met Thr Asp Phe  
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Ser Asp Tyr Leu Arg Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly	
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Tyr Tyr Val Ser Leu Ala Tyr Asp Ile Tyr Lys Ser Tyr Asp Ala Tyr	
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Asp Leu Ser Thr His Asp Gln Ala Leu Pro His Leu Leu Ser Ala Lys	
190 195 200	

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Glu Ser Ala Glu Asp Ile Gln Asn Lys Ala Ile Val Ala Lys Ala Leu	
205 210 215	
tta aat gta gca tat tgt tat aat gca atg gag aga cca aca aaa gct	1205
Leu Asn Val Ala Tyr Cys Tyr Asn Ala Met Glu Arg Pro Thr Lys Ala	
220 225 230 235	
att gaa tac ttt cat aag gcg att gat gta gca aag gaa ata aag gca	1253
Ile Glu Tyr Phe His Lys Ala Ile Asp Val Ala Lys Glu Ile Lys Ala	
240 245 250	
aaa gaa ctg act cag gct tat tat gat ttg gca tta att cac ttt cga	1301
Lys Glu Leu Thr Gln Ala Tyr Tyr Asp Leu Ala Leu Ile His Phe Arg	
255 260 265	
aat aac gaa aat att gaa gga cga aaa ttt tat gaa aag gcg ctt gaa	1349
Asn Asn Glu Asn Ile Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu	
270 275 280	
agt gcg cgg gta ttt gaa gat gaa tta ttc ctg tgt ctg ttg gat gtt	1397
Ser Ala Arg Val Phe Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val	
285 290 295	
tta gag gca ctg ttt ata aaa tca gct aat aag tca gag gta cta gaa	1445
Leu Glu Ala Leu Phe Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu	
300 305 310 315	
aca atg aaa cca tta cgg gat agt cgt ggt tac ccc tat ctt gag gaa	1493
Thr Met Lys Pro Leu Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu	
320 325 330	
ctg gca tta gaa gca gct cta ttc tat act agg aat gag cgg cca aat	1541
Leu Ala Leu Glu Ala Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn	
335 340 345	
gat tcc ata ttt ttt tat gat cag atg gtg cag gct cag aaa caa atc	1589
Asp Ser Ile Phe Phe Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile	
350 355 360	
aaa agg ggc gac ttt ctg tat gaa atc taagctgttt ctttcgctga	1636
Lys Arg Gly Asp Phe Leu Tyr Glu Ile	
365 370	
cccttgcttt gggcttggtg gtcgtgtcga gcgcttccat tcacacatct gttgaacaac	1696
aacatgcaga attttctgta gcatctaggc tcgcaacata attgtgtttg ggcagggtcat	1756
gtgatggcct gccttttttg tgaaagaatt attttagttt gaaaaccaga acgattgtgt	1816
taatactcat ctttcttcgt cccttggtgtt ggaattttca tcatatcaat atttgaatat	1876
gcggctgtcc gcattattaa caattttaaa ttttttgcac aaattttata caaaggcaga	1936
caaaaacctt gatatatcaa tggttctatg ggtatatcca accacgacca ccgatatcgc	1996

taaaaaccgt attgccaaac gacgaaagag cgttccttac acaaggaatg ctctttttgt 2056

ttattcctca tcaaagcgga gagccgcaa cataaacgca atgaccaact gttgtccgc 2115

<210> 32

<211> 372

<212> PRT

<213> Bacillus licheniformis

<400> 32

Leu Glu Thr Ile Pro Ser Ser Glu Val Gly Ile Lys Ile Asn Arg Trp  
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Tyr Asn Glu Ile Gln Lys Leu Asn Val Ile Glu Ala Glu Arg Leu Lys  
20 25 30

Ala Glu Val His Leu Ala Ile Glu Arg Met Glu Glu Asp Gln Asp Leu  
35 40 45

Leu Ser Tyr Tyr Gln Leu Met Asn Phe Arg His Glu Leu Met Leu Glu  
50 55 60

Tyr Leu Phe Pro Ala Glu Lys Lys Leu Ser Lys Ser Asp Tyr Leu Arg  
65 70 75 80

Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly Leu Leu Glu Tyr Tyr  
85 90 95

Phe Ser Phe Phe Thr Gly Met Tyr His Phe Ser Arg Gly Lys Tyr Ile  
100 105 110

Lys Ala Ile Lys Ala Tyr Arg Ala Ala Glu Lys Lys Leu Thr Lys Val  
115 120 125

Ser Asp Lys Ile Glu Lys Ala Glu Phe Tyr Tyr Lys Met Ala Glu Val  
130 135 140

Phe Tyr His Met Lys Gln Thr His Met Ser Met Tyr Tyr Val Ser Leu  
145 150 155 160

Ala Tyr Asp Ile Tyr Lys Ser Tyr Asp Ala Tyr Val Ile Arg Arg Ile  
165 170 175

Asn Cys Leu Phe Val Val Ala Gly Asn Tyr Ile Asp Leu Ser Thr His

180	185	190
Asp Gln Ala Leu Pro His Leu Leu Ser Ala Lys Glu Ser Ala Glu Asp 195 200 205		
Ile Gln Asn Lys Ala Ile Val Ala Lys Ala Leu Leu Asn Val Ala Tyr 210 215 220		
Cys Tyr Asn Ala Met Glu Arg Pro Thr Lys Ala Ile Glu Tyr Phe His 225 230 235 240		
Lys Ala Ile Asp Val Ala Lys Glu Ile Lys Ala Lys Glu Leu Thr Gln 245 250 255		
Ala Tyr Tyr Asp Leu Ala Leu Ile His Phe Arg Asn Asn Glu Asn Ile 260 265 270		
Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu Ser Ala Arg Val Phe 275 280 285		
Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val Leu Glu Ala Leu Phe 290 295 300		
Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu Thr Met Lys Pro Leu 305 310 315 320		
Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu Leu Ala Leu Glu Ala 325 330 335		
Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn Asp Ser Ile Phe Phe 340 345 350		
Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile Lys Arg Gly Asp Phe 355 360 365		
Leu Tyr Glu Ile 370		

<210> 33  
 <211> 2077  
 <212> DNA  
 <213> Bacillus licheniformis

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<222> (501)..(1574)

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tatagtaaag cgaatagagg agggatataca aatgaatcct tactatatga tgctcttatg 180
ttatgtccta tcgatcatcc actttttaat aggctaccgg gaagccctga aaataagcgg 240
ggttgacggg ctgggtcaacg gaaccgcaat gatctcctgt attccgcttg gcgcgggttt 300
cgcttttttc gcgcactttt tttggaaaat gacgatttaa tttcggaat gaattttttc 360
gccacaac atgcatttcc gtgttattca cagacggcgg cagtttatgc tatgattaat 420
agaacttcaa ttacaaaaa attcacaaag attggaggga aaagaatggc caaagccggg 480
cttctcaaga agtcgccaat atg ctg aac gac tgg tac ata ctg atg aaa aaa 533
Met Leu Asn Asp Trp Tyr Ile Leu Met Lys Lys
1 5 10

cga gac att tca ggt tca atc gaa atg aaa gat gac ata gat aaa gca 581
Arg Asp Ile Ser Gly Ser Ile Glu Met Lys Asp Asp Ile Asp Lys Ala
15 20 25

att gaa aag atg gaa gaa gat cat gac gtt ctt ctc tat tat caa atg 629
Ile Glu Lys Met Glu Glu Asp His Asp Val Leu Leu Tyr Tyr Gln Met
30 35 40

ctg gat ttt cgc tta agg ctt ctt ctt gaa gat atc tcc caa tct tcc 677
Leu Asp Phe Arg Leu Arg Leu Leu Leu Glu Asp Ile Ser Gln Ser Ser
45 50 55

aca gaa aaa ttg gaa gcc atc agt ttt aag gac aaa gat cca aaa agt 725
Thr Glu Lys Leu Glu Ala Ile Ser Phe Lys Asp Lys Asp Pro Lys Ser
60 65 70 75

acg gac gat aag ctg aat tat tat ttt tat ctg ttc aaa ggg att tat 773
Thr Asp Asp Lys Leu Asn Tyr Tyr Phe Tyr Leu Phe Lys Gly Ile Tyr
80 85 90

gaa gac tac aag caa aac cat aca gaa gcg ctt aat ttt ttc aga ata 821
Glu Asp Tyr Lys Gln Asn His Thr Glu Ala Leu Asn Phe Phe Arg Ile
95 100 105

gcg gaa aaa agg ctg agc gtc att caa aat gaa att gaa aaa gcc gaa 869
Ala Glu Lys Arg Leu Ser Val Ile Gln Asn Glu Ile Glu Lys Ala Glu
110 115 120

ttt cat tat aaa atc ggt gtt ttg tat tac aac tta aaa gcg aca tgg 917
Phe His Tyr Lys Ile Gly Val Leu Tyr Tyr Asn Leu Lys Ala Thr Trp
125 130 135

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ctg tcg att cac cac atc aac att gcc tca ggc atc ttc caa ggg tat	965
Leu Ser Ile His His Ile Asn Ile Ala Ser Gly Ile Phe Gln Gly Tyr	
140 145 150 155	
gac ggg tat gcc aag cgg gtc atc aac tgc aaa atg ctg atc ggg ctc	1013
Asp Gly Tyr Ala Lys Arg Val Ile Asn Cys Lys Met Leu Ile Gly Leu	
160 165 170	
aat tat att gac caa ttt aag ttt gcc gaa agt gaa gta ttg tta aag	1061
Asn Tyr Ile Asp Gln Phe Lys Phe Ala Glu Ser Glu Val Leu Leu Lys	
175 180 185	
gaa gca att gaa aaa acc gaa aaa atc ggc gac caa tat ctt ttg cct	1109
Glu Ala Ile Glu Lys Thr Glu Lys Ile Gly Asp Gln Tyr Leu Leu Pro	
190 195 200	
tat acc tac tat aat atg ggc ttt ttg aag agt aag gaa gat aaa cac	1157
Tyr Thr Tyr Tyr Asn Met Gly Phe Leu Lys Ser Lys Glu Asp Lys His	
205 210 215	
gaa gaa gcg ctg aag tat tat aat aaa gct ttt gca atc aaa gac ttt	1205
Glu Glu Ala Leu Lys Tyr Tyr Asn Lys Ala Phe Ala Ile Lys Asp Phe	
220 225 230 235	
gaa acg aaa gcc aag tat gct tac ctt cta tgt gta tat gaa aac aca	1253
Glu Thr Lys Ala Lys Tyr Ala Tyr Leu Leu Cys Val Tyr Glu Asn Thr	
240 245 250	
agg tct ctt ttc aaa acc aac gat ccc gac caa gct ttt aaa tgg atc	1301
Arg Ser Leu Phe Lys Thr Asn Asp Pro Asp Gln Ala Phe Lys Trp Ile	
255 260 265	
gac aca ggc ttt aaa aaa gct caa gaa gtg aat agc gaa att ttc gaa	1349
Asp Thr Gly Phe Lys Lys Ala Gln Glu Val Asn Ser Glu Ile Phe Glu	
270 275 280	
tta aaa ttc aaa act tta tat aca tta cat tcc gat tgt cag aat aaa	1397
Leu Lys Phe Lys Thr Leu Tyr Thr Leu His Ser Asp Cys Gln Asn Lys	
285 290 295	
ctg gaa gta atc aag gac ttt att cac caa tta gaa gat aaa aaa gca	1445
Leu Glu Val Ile Lys Asp Phe Ile His Gln Leu Glu Asp Lys Lys Ala	
300 305 310 315	
tgg gtt gat ctg gag gaa ttg ctg atg gac gta gcg aat tac tat agg	1493
Trp Val Asp Leu Glu Glu Leu Leu Met Asp Val Ala Asn Tyr Tyr Arg	
320 325 330	
gaa aat aag tta tac gaa gaa gcc ata tat ttc tac att aaa aca gac	1541
Glu Asn Lys Leu Tyr Glu Glu Ala Ile Tyr Phe Tyr Ile Lys Thr Asp	
335 340 345	
aag gca agt aaa ctt gcc gga aga gga gga gaa taggatgaaa aaagtgttgt	1594
Lys Ala Ser Lys Leu Ala Gly Arg Gly Gly Glu	
350 355	
tagctgtatt tgtattaggc actgttttca gcttttcggt tgcaaatcac gctcctgaag	1654

cggttccca aagcaatgag atacttttgg cttctcgtgg agcaggcggg tgactacatc 1714  
 ctcaaaatac ccattcagac atctgctgaa tgggtatttt gcactttaca ttcataattca 1774  
 ggagtgatcg atatgggaaa gaaagtactg ctgacaggat ttgacccctt tgggggagaa 1834  
 acagtcaatc cgtcctggga agctgtaaaa cggtgaacg gagaggaagc agaaggcgtc 1894  
 tctatcgcag cggagcagat tccgaccgtt tttcatcatt cagcggccgt tttgaaaaaa 1954  
 gcgatcgaaa agcacaaacc cgatgtcgtc atttgcgcag ggcaagcagg cggcagggct 2014  
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 gac 2077

<210> 34  
 <211> 358  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 34

Met Leu Asn Asp Trp Tyr Ile Leu Met Lys Lys Arg Asp Ile Ser Gly  
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Ser Ile Glu Met Lys Asp Asp Ile Asp Lys Ala Ile Glu Lys Met Glu  
 20 25 30

Glu Asp His Asp Val Leu Leu Tyr Tyr Gln Met Leu Asp Phe Arg Leu  
 35 40 45

Arg Leu Leu Leu Glu Asp Ile Ser Gln Ser Ser Thr Glu Lys Leu Glu  
 50 55 60

Ala Ile Ser Phe Lys Asp Lys Asp Pro Lys Ser Thr Asp Asp Lys Leu  
 65 70 75 80

Asn Tyr Tyr Phe Tyr Leu Phe Lys Gly Ile Tyr Glu Asp Tyr Lys Gln  
 85 90 95

Asn His Thr Glu Ala Leu Asn Phe Phe Arg Ile Ala Glu Lys Arg Leu  
 100 105 110

Ser Val Ile Gln Asn Glu Ile Glu Lys Ala Glu Phe His Tyr Lys Ile  
 115 120 125



Gly Val Leu Tyr Tyr Asn Leu Lys Ala Thr Trp Leu Ser Ile His His  
 130 135 140

Ile Asn Ile Ala Ser Gly Ile Phe Gln Gly Tyr Asp Gly Tyr Ala Lys  
 145 150 155 160

Arg Val Ile Asn Cys Lys Met Leu Ile Gly Leu Asn Tyr Ile Asp Gln  
 165 170 175

Phe Lys Phe Ala Glu Ser Glu Val Leu Leu Lys Glu Ala Ile Glu Lys  
 180 185 190

Thr Glu Lys Ile Gly Asp Gln Tyr Leu Leu Pro Tyr Thr Tyr Tyr Asn  
 195 200 205

Met Gly Phe Leu Lys Ser Lys Glu Asp Lys His Glu Glu Ala Leu Lys  
 210 215 220

Tyr Tyr Asn Lys Ala Phe Ala Ile Lys Asp Phe Glu Thr Lys Ala Lys  
 225 230 235 240

Tyr Ala Tyr Leu Leu Cys Val Tyr Glu Asn Thr Arg Ser Leu Phe Lys  
 245 250 255

Thr Asn Asp Pro Asp Gln Ala Phe Lys Trp Ile Asp Thr Gly Phe Lys  
 260 265 270

Lys Ala Gln Glu Val Asn Ser Glu Ile Phe Glu Leu Lys Phe Lys Thr  
 275 280 285

Leu Tyr Thr Leu His Ser Asp Cys Gln Asn Lys Leu Glu Val Ile Lys  
 290 295 300

Asp Phe Ile His Gln Leu Glu Asp Lys Lys Ala Trp Val Asp Leu Glu  
 305 310 315 320

Glu Leu Leu Met Asp Val Ala Asn Tyr Tyr Arg Glu Asn Lys Leu Tyr  
 325 330 335

Glu Glu Ala Ile Tyr Phe Tyr Ile Lys Thr Asp Lys Ala Ser Lys Leu  
 340 345 350

Ala Gly Arg Gly Gly Glu

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<210> 35
<211> 2101
<212> DNA
<213> Bacillus licheniformis
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<220>
<221> CDS
<222> (501) .. (1598)
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54

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Gln Ala Ile Ser Phe Tyr Lys Ile Ala Glu Lys Lys Leu Ala His Val	
110 115 120	
cat gat gaa att gag gtg gcg caa ttt cac gat aaa gtc gga aag ctc	917
His Asp Glu Ile Glu Val Ala Gln Phe His Asp Lys Val Gly Lys Leu	
125 130 135	
tac tat tac ttg ggc cag aat atc gtc tct tta aac cat acc cgg cag	965
Tyr Tyr Tyr Leu Gly Gln Asn Ile Val Ser Leu Asn His Thr Arg Gln	
140 145 150 155	
gcg atg gaa att ttc aag ggg cat ggc gac cat gat atg aac ctt gtt	1013
Ala Met Glu Ile Phe Lys Gly His Gly Asp His Asp Met Asn Leu Val	
160 165 170	
tcc act tat att acg atg gcc gga aat tat aca gag atg ggg aaa tat	1061
Ser Thr Tyr Ile Thr Met Ala Gly Asn Tyr Thr Glu Met Gly Lys Tyr	
175 180 185	
aca gag gcg gaa gaa tat tta aca gaa gcc atc cat acg gta aga aaa	1109
Thr Glu Ala Glu Glu Tyr Leu Thr Glu Ala Ile His Thr Val Arg Lys	
190 195 200	
gcc ggc gac tgt ttt aaa gaa atg cag ctc ctt cat aat ttt gcc ttg	1157
Ala Gly Asp Cys Phe Lys Glu Met Gln Leu Leu His Asn Phe Ala Leu	
205 210 215	
ctt tat gcg gcg atg gac aat tcg gaa aaa agc att cag ttt tta gaa	1205
Leu Tyr Ala Ala Met Asp Asn Ser Glu Lys Ser Ile Gln Phe Leu Glu	
220 225 230 235	
atc gtt ttg gat gat caa gca tat gct gca tca gat tat tat ttc aat	1253
Ile Val Leu Asp Asp Gln Ala Tyr Ala Ala Ser Asp Tyr Tyr Phe Asn	
240 245 250	
gct gtg ttt tta atg atc aaa gag ctg ttt aaa gtc gga gac cat aaa	1301
Ala Val Phe Leu Met Ile Lys Glu Leu Phe Lys Val Gly Asp His Lys	
255 260 265	
cgc gct gca gcc ttt tac aaa gaa ggg aag gaa agg tcg aaa tcc gcg	1349
Arg Ala Ala Ala Phe Tyr Lys Glu Gly Lys Glu Arg Ser Lys Ser Ala	
270 275 280	
gcg aat aaa ata ttt gac gcc aaa atc gat att tta tat gcg gct tat	1397
Ala Asn Lys Ile Phe Asp Ala Lys Ile Asp Ile Leu Tyr Ala Ala Tyr	
285 290 295	
gca gga gat ggt gaa cag gcg gtt aaa gac tgc aaa gac aac att gaa	1445
Ala Gly Asp Gly Glu Gln Ala Val Lys Asp Cys Lys Asp Asn Ile Glu	
300 305 310 315	
atc ctg ttt caa aca aag caa tac gac agc gcc aga gaa ctt tcg ctc	1493
Ile Leu Phe Gln Thr Lys Gln Tyr Asp Ser Ala Arg Glu Leu Ser Leu	
320 325 330	

tta acg gcc aat gtt tac aga tca aag tca ctt tat aaa gaa gcc gca 1541  
 Leu Thr Ala Asn Val Tyr Arg Ser Lys Ser Leu Tyr Lys Glu Ala Ala  
 335 340 345  
 cat ttc ttt ttg gaa gcg att aaa gcg gaa gaa aaa atg aaa aaa gtg 1589  
 His Phe Phe Leu Glu Ala Ile Lys Ala Glu Glu Lys Met Lys Lys Val  
 350 355 360  
 gag gga atg tgatgaaaaa actgttcatt gttgctgoga ttgctgccgt 1638  
 Glu Gly Met  
 365  
 cgtatgttcg ggatggtttg cggcagaaac tcaactgggca tccggcgaca tgcagggttgc 1698  
 tgaaaagatg gtcgggttaa tcgaatactc ggaacaaata tgaacatccg ctcctgagca 1758  
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 atgaacactt cttcaccact atttaggggtg gtcaacctaa acaaaggtag gaaacctgtg 1878  
 ctgactactt ttactccgat gtcctttcag ctattcttgt cagtaagatc attccccatc 1938  
 tcttcaacgc ctcaggcatc acctattaaa aaaatcataa ttgaaacttg tcagcaaata 1998  
 tgttgcataa caccaggatg tttccacaat aattaacat taagactttt ttgacttcca 2058  
 gaaggaagaa caagatattt atgtaaaatc actcttttat tca 2101

<210> 36  
 <211> 366  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 36

Met Asn Lys Ile Ala Ala Glu Glu Val Ala Asn Ile Leu Asn Thr Trp  
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Tyr Arg Ala Ile Arg Arg Asn Asp Ala Glu Gln Ser Ile Arg Ile Phe  
 20 25 30

Glu Glu Val Lys Pro Met Leu Ala Glu Met Glu Glu Asp Gln Glu Val  
 35 40 45

Leu Ile Tyr Tyr Ser Leu Leu Glu Leu Arg His Lys Ile Met Leu Tyr  
 50 55 60

Asp Thr Arg Gly Lys Lys Ile Glu Gln Gln Glu Glu Leu Thr Asn Gly  
 65 70 75 80

Gly Ser Ala Ala Ser His Met Thr Ser Tyr Tyr Tyr Tyr Leu Phe Ser

85										90					95				
Gly	Ala	Tyr	Glu	Val	Tyr	Lys	Lys	Asn	Tyr	Glu	Gln	Ala	Ile	Ser	Phe				
			100					105					110						
Tyr	Lys	Ile	Ala	Glu	Lys	Lys	Leu	Ala	His	Val	His	Asp	Glu	Ile	Glu				
		115					120					125							
Val	Ala	Gln	Phe	His	Asp	Lys	Val	Gly	Lys	Leu	Tyr	Tyr	Tyr	Leu	Gly				
	130					135					140								
Gln	Asn	Ile	Val	Ser	Leu	Asn	His	Thr	Arg	Gln	Ala	Met	Glu	Ile	Phe				
145					150					155					160				
Lys	Gly	His	Gly	Asp	His	Asp	Met	Asn	Leu	Val	Ser	Thr	Tyr	Ile	Thr				
			165					170						175					
Met	Ala	Gly	Asn	Tyr	Thr	Glu	Met	Gly	Lys	Tyr	Thr	Glu	Ala	Glu	Glu				
		180						185					190						
Tyr	Leu	Thr	Glu	Ala	Ile	His	Thr	Val	Arg	Lys	Ala	Gly	Asp	Cys	Phe				
	195						200					205							
Lys	Glu	Met	Gln	Leu	Leu	His	Asn	Phe	Ala	Leu	Leu	Tyr	Ala	Ala	Met				
	210					215					220								
Asp	Asn	Ser	Glu	Lys	Ser	Ile	Gln	Phe	Leu	Glu	Ile	Val	Leu	Asp	Asp				
225					230					235					240				
Gln	Ala	Tyr	Ala	Ala	Ser	Asp	Tyr	Tyr	Phe	Asn	Ala	Val	Phe	Leu	Met				
			245						250					255					
Ile	Lys	Glu	Leu	Phe	Lys	Val	Gly	Asp	His	Lys	Arg	Ala	Ala	Ala	Phe				
		260					265						270						
Tyr	Lys	Glu	Gly	Lys	Glu	Arg	Ser	Lys	Ser	Ala	Ala	Asn	Lys	Ile	Phe				
	275						280					285							
Asp	Ala	Lys	Ile	Asp	Ile	Leu	Tyr	Ala	Ala	Tyr	Ala	Gly	Asp	Gly	Glu				
	290					295					300								
Gln	Ala	Val	Lys	Asp	Cys	Lys	Asp	Asn	Ile	Glu	Ile	Leu	Phe	Gln	Thr				
305					310					315					320				

Lys Gln Tyr Asp Ser Ala Arg Glu Leu Ser Leu Leu Thr Ala Asn Val  
325 330 335

Tyr Arg Ser Lys Ser Leu Tyr Lys Glu Ala Ala His Phe Phe Leu Glu  
340 345 350

Ala Ile Lys Ala Glu Glu Lys Met Lys Lys Val Glu Gly Met  
355 360 365

<210> 37  
<211> 1936  
<212> DNA  
<213> Bacillus licheniformis

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<222> (384)..(1433)

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tttgacaatg aacagaatcg acatgccgca tttgctgtgg tcgctggagc agatcgacaa 180  
agggtgaaccg acaggcgtga tcaaagtgga tcaagatatt gcaaaagatg ccattcttgc 240  
gctgaatcgg atgttaacga tccgttaact ttttgagagaa caagttttta tcataacccc 300  
tccgctatgc gcataaattt gtggagaagc atatttgta ttctcatctg ttcgttcacg 360  
tttttgcata ggaggggaaa acg ttg aaa att cat att gtc caa aag ggc gat 413  
Leu Lys Ile His Ile Val Gln Lys Gly Asp  
1 5 10  
tct ctg gaa aaa atc gcg gaa aga tat gaa gtg gac ttt gaa gaa ctg 461  
Ser Leu Glu Lys Ile Ala Glu Arg Tyr Glu Val Asp Phe Glu Glu Leu  
15 20 25  
aaa aag ctg aat tcg cag ctg agc aat cca gac ttg atc atg ccg ggc 509  
Lys Lys Leu Asn Ser Gln Leu Ser Asn Pro Asp Leu Ile Met Pro Gly  
30 35 40  
atg aaa atc aaa gta ccg tca ggg gga gtg ccg gtc aaa aaa gaa gaa 557  
Met Lys Ile Lys Val Pro Ser Gly Gly Val Pro Val Lys Lys Glu Glu  
45 50 55  
cag ctc aat atg cga aag gaa tta ccg aaa aaa cag cag gaa cat cca 605  
Gln Leu Asn Met Arg Lys Glu Leu Pro Lys Lys Gln Gln Glu His Pro  
60 65 70

ttt gca aaa gaa aag ccg aaa agc aag ctt gat gtt gaa gat ata aaa	653
Phe Ala Lys Glu Lys Pro Lys Ser Lys Leu Asp Val Glu Asp Ile Lys	
75 80 85 90	
ccg aaa gaa aag cct tcg gtt cct tat gtt ccg cct gtc ccg aac atc	701
Pro Lys Glu Lys Pro Ser Val Pro Tyr Val Pro Pro Val Pro Asn Ile	
95 100 105	
gga caa tca agt ttg cct gaa ggc gac att tcg aat ttg tat caa agc	749
Gly Gln Ser Ser Leu Pro Glu Gly Asp Ile Ser Asn Leu Tyr Gln Ser	
110 115 120	
gtc aat cag ctt cat cag ccg tac gta cct cca aaa cct tat gaa cat	797
Val Asn Gln Leu His Gln Pro Tyr Val Pro Pro Lys Pro Tyr Glu His	
125 130 135	
caa gag aaa ggc ccc aac atg tat aat cca tgg aca aat gag gag gaa	845
Gln Glu Lys Gly Pro Asn Met Tyr Asn Pro Trp Thr Asn Glu Glu Glu	
140 145 150	
aac cat atg gaa aat gtc aat tat ccg aat gtt ccg cag ccg cca aat	893
Asn His Met Glu Asn Val Asn Tyr Pro Asn Val Pro Gln Pro Pro Asn	
155 160 165 170	
gtc ggt gca gca ggt gat gaa aat aag cag ttt cac ggc atg ccg aat	941
Val Gly Ala Ala Gly Asp Glu Asn Lys Gln Phe His Gly Met Pro Asn	
175 180 185	
gta gct gca gcg gga tat cat cac cat cca tat cct tat ccg ttc tat	989
Val Ala Ala Ala Gly Tyr His His His Pro Tyr Pro Tyr Pro Phe Tyr	
190 195 200	
cct gga ggc tgc tgg att cct gtt tca ccg gtg ctg cct gga tgc gga	1037
Pro Gly Gly Cys Trp Ile Pro Val Ser Pro Val Leu Pro Gly Ser Gly	
205 210 215	
ttg tgc cat cct tgg tat cca tat cct gct caa atg cct tat atg cat	1085
Leu Cys His Pro Trp Tyr Pro Tyr Pro Ala Gln Met Pro Tyr Met His	
220 225 230	
cag cct agc tat gta tct cct gct gaa tat gac gat gat gac aac atg	1133
Gln Pro Ser Tyr Val Ser Pro Ala Glu Tyr Asp Asp Asp Asp Asn Met	
235 240 245 250	
ggg cat gac aat gcc ggt cat cac gga tac cat cat cag ccg atg act	1181
Gly His Asp Asn Ala Gly His His Gly Tyr His His Gln Pro Met Thr	
255 260 265	
gcc ccg gca tat gcg cct tac cag ccg ttc ccg gga ttt gca ccg cca	1229
Ala Pro Ala Tyr Ala Pro Tyr Gln Pro Phe Pro Gly Phe Ala Pro Pro	
270 275 280	
aac gtc ggt cac gcc ggg gac cct aat atg gca cac ggc aaa gaa gat	1277
Asn Val Gly His Ala Gly Asp Pro Asn Met Ala His Gly Lys Glu Asp	
285 290 295	
gac tgc ggg tgc ggg ccg ggc caa ttc ccg gga ggt ttt cca ggt gcg	1325

Asp Cys Gly Cys Gly Pro Gly Gln Phe Pro Gly Gly Phe Pro Gly Ala  
 300 305 310  
 gcg cca tat gga cag atg ccg caa atg gga gct ccg tac ggt atg ggg 1373  
 Ala Pro Tyr Gly Gln Met Pro Gln Met Gly Ala Pro Tyr Gly Met Gly  
 315 320 325 330  
 gga tac gga cag cag cct gca ggg gga cag atg ttt aac aga ccg gaa 1421  
 Gly Tyr Gly Gln Gln Pro Ala Gly Gly Gln Met Phe Asn Arg Pro Glu  
 335 340 345  
 gat gat gaa gac tgattcggaa tgggacgatg atctatcggt ccttttttat 1473  
 Asp Asp Glu Asp  
 350  
 tgtggaccgc tataaacatt ttcattgctat ttaacgggaa tgtctataac tgtcaagggt 1533  
 aactcttcgc atcccgcaaca tcctaaaaaa gagcgcaatg ctcaaattca gcggtttttca 1593  
 cgggggggtac taccattgga cagcaagctg aaagtgtttt cggggattttt gctttttgaca 1653  
 gcaggtctat ctgcatgcgg aacgaacgac gctatagata atggaaacaa tacgcgccccg 1713  
 atcggatatt atctcaaatg atgcagatcg taatgcaggg tcttgataat gacggccctg 1773  
 ttacagaaat gcttgaaaac atgaacggga gacacgggtgc aacaaacgta aacaatcgag 1833  
 cgggaaacgg caatcccggt ccaacaggcg atggaactta cagccgggga gacatgaatt 1893  
 atcacaacca tttggtgaat acggcgggata caggctatga cag 1936

<210> 38  
 <211> 350  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 38

Leu Lys Ile His Ile Val Gln Lys Gly Asp Ser Leu Glu Lys Ile Ala  
 1 5 10 15

Glu Arg Tyr Glu Val Asp Phe Glu Glu Leu Lys Lys Leu Asn Ser Gln  
 20 25 30

Leu Ser Asn Pro Asp Leu Ile Met Pro Gly Met Lys Ile Lys Val Pro  
 35 40 45

Ser Gly Gly Val Pro Val Lys Lys Glu Glu Gln Leu Asn Met Arg Lys  
 50 55 60

Glu Leu Pro Lys Lys Gln Gln Glu His Pro Phe Ala Lys Glu Lys Pro  
 65 70 75 80



Lys Ser Lys Leu Asp Val Glu Asp Ile Lys Pro Lys Glu Lys Pro Ser  
 85 90 95

Val Pro Tyr Val Pro Pro Val Pro Asn Ile Gly Gln Ser Ser Leu Pro  
 100 105 110

Glu Gly Asp Ile Ser Asn Leu Tyr Gln Ser Val Asn Gln Leu His Gln  
 115 120 125

Pro Tyr Val Pro Pro Lys Pro Tyr Glu His Gln Glu Lys Gly Pro Asn  
 130 135 140

Met Tyr Asn Pro Trp Thr Asn Glu Glu Glu Asn His Met Glu Asn Val  
 145 150 155 160

Asn Tyr Pro Asn Val Pro Gln Pro Pro Asn Val Gly Ala Ala Gly Asp  
 165 170 175

Glu Asn Lys Gln Phe His Gly Met Pro Asn Val Ala Ala Ala Gly Tyr  
 180 185 190

His His His Pro Tyr Pro Tyr Pro Phe Tyr Pro Gly Gly Cys Trp Ile  
 195 200 205

Pro Val Ser Pro Val Leu Pro Gly Ser Gly Leu Cys His Pro Trp Tyr  
 210 215 220

Pro Tyr Pro Ala Gln Met Pro Tyr Met His Gln Pro Ser Tyr Val Ser  
 225 230 235 240

Pro Ala Glu Tyr Asp Asp Asp Asp Asn Met Gly His Asp Asn Ala Gly  
 245 250 255

His His Gly Tyr His His Gln Pro Met Thr Ala Pro Ala Tyr Ala Pro  
 260 265 270

Tyr Gln Pro Phe Pro Gly Phe Ala Pro Pro Asn Val Gly His Ala Gly  
 275 280 285

Asp Pro Asn Met Ala His Gly Lys Glu Asp Asp Cys Gly Cys Gly Pro  
 290 295 300

Gly Gln Phe Pro Gly Gly Phe Pro Gly Ala Ala Pro Tyr Gly Gln Met  
 305 310 315 320

Pro Gln Met Gly Ala Pro Tyr Gly Met Gly Gly Tyr Gly Gln Gln Pro  
 325 330 335

Ala Gly Gly Gln Met Phe Asn Arg Pro Glu Asp Asp Glu Asp  
 340 345 350

<210> 39  
 <211> 2027  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1526)

<400> 39  
 aagagcaaat tctgtctatg agcacaacag aagaggttgt acaattcgta aaagaaacct 60  
 tcaacctggc ataagcaatt gaaaatccgg accggcatca ccaatgcccg tccgggtttt 120  
 ttgtttatct gaatgatccc ggctgcggcg gagataatac atgtgaccaa ttgttagaaa 180  
 gggggattct gatatgccta ggcagccatt caaactggga gatgaggtgt atgtcattta 240  
 ccggaatccg catgcagcga atgtggcgca tataaaggaa gctgaagtcg ttgatcatcc 300  
 gcttcacgaa ggcgaactgg cattgtttat gtatgataca tatcacgcct ttgccgaaga 360  
 tgatgccgtt ttttcttcat atgaagaggc ggaacggctt taccgtgaat tatttgacgg 420  
 gatatgaaga cattaccggt atatcacatc ctctaaatgc aaaaagtaat ggaaatatgc 480  
 aaaggatgtg tctgtttcca atg gta aaa ccg ttt gtt ccc caa ctc gtc tat 533  
 Met Val Lys Pro Phe Val Pro Gln Leu Val Tyr  
 1 5 10  
 att gaa ccg aga gcc ctg gaa tat ccg ctt gga aaa gag ctg agg gat 581  
 Ile Glu Pro Arg Ala Leu Glu Tyr Pro Leu Gly Lys Glu Leu Arg Asp  
 15 20 25  
 aaa ttt tca aac atg gga ctt gag atc agg gaa aca act tca cac aac 629  
 Lys Phe Ser Asn Met Gly Leu Glu Ile Arg Glu Thr Thr Ser His Asn  
 30 35 40  
 cag gtg agg aat atc ccg ggg gaa ggc cac ctg caa aaa tac aga aat 677  
 Gln Val Arg Asn Ile Pro Gly Glu Gly His Leu Gln Lys Tyr Arg Asn  
 45 50 55  
 gcg aaa tcc act ttg gtg atc ggc gtc aga aaa aca ttg aag ttc gat 725

Ala Lys Ser Thr Leu Val Ile Gly Val Arg Lys Thr Leu Lys Phe Asp	
60 65 70 75	
tcg tca aaa ccg tcc gca gaa tac gcg atc ccg ttt gca aca ggg tgt	773
Ser Ser Lys Pro Ser Ala Glu Tyr Ala Ile Pro Phe Ala Thr Gly Cys	
80 85 90	
atg ggt cac tgt cat tac tgc tac ctg caa acg aca atg ggc agc aag	821
Met Gly His Cys His Tyr Cys Tyr Leu Gln Thr Thr Met Gly Ser Lys	
95 100 105	
ccg tat atc aga acg tac gtc aat gtg gag gaa ata ctt gag cag gcg	869
Pro Tyr Ile Arg Thr Tyr Val Asn Val Glu Glu Ile Leu Glu Gln Ala	
110 115 120	
gat caa tat ata aaa gaa agg gct ccc gaa gat acg cgg ttt gaa gct	917
Asp Gln Tyr Ile Lys Glu Arg Ala Pro Glu Asp Thr Arg Phe Glu Ala	
125 130 135	
tcc tgc aca tcc gat atc gtc gga att gac cat ttg aca cat acg tta	965
Ser Cys Thr Ser Asp Ile Val Gly Ile Asp His Leu Thr His Thr Leu	
140 145 150 155	
aaa cgc gcc att gag cat ttc ggt caa acc gac cat ggt aag ctg cgt	1013
Lys Arg Ala Ile Glu His Phe Gly Gln Thr Asp His Gly Lys Leu Arg	
160 165 170	
ttc gtg aca aaa ttt cat cat gtc gac cat ttg ctc gat gcc aag cac	1061
Phe Val Thr Lys Phe His His Val Asp His Leu Leu Asp Ala Lys His	
175 180 185	
aac gga aaa acg cgc ttc cgc ttc agc gtg aat gcc gaa tat gtc att	1109
Asn Gly Lys Thr Arg Phe Arg Phe Ser Val Asn Ala Glu Tyr Val Ile	
190 195 200	
aaa agc ttt gaa ccc ggc aca tcc ccg ttg gat aaa cgg atc gaa gcc	1157
Lys Ser Phe Glu Pro Gly Thr Ser Pro Leu Asp Lys Arg Ile Glu Ala	
205 210 215	
gcc gtg aaa gta gcg gaa gcg ggc tat ccg ctc ggt ttt atc atc gct	1205
Ala Val Lys Val Ala Glu Ala Gly Tyr Pro Leu Gly Phe Ile Ile Ala	
220 225 230 235	
ccg att tat att cat gac ggc tgg cag gaa ggc tac aga gtt ctg ctg	1253
Pro Ile Tyr Ile His Asp Gly Trp Gln Glu Gly Tyr Arg Val Leu Leu	
240 245 250	
gaa aag ctc gat cgt gcg ctg ccg cag cat gcg agg cgc gac atc acc	1301
Glu Lys Leu Asp Arg Ala Leu Pro Gln His Ala Arg Arg Asp Ile Thr	
255 260 265	
ttt gaa atg atc cag cat aga ttc acg aag ccg gca aag aga gtc att	1349
Phe Glu Met Ile Gln His Arg Phe Thr Lys Pro Ala Lys Arg Val Ile	
270 275 280	
gaa aaa aac tat cca aag aca aag ctc gaa ctg gat gaa gaa aaa cgg	1397
Glu Lys Asn Tyr Pro Lys Thr Lys Leu Glu Leu Asp Glu Glu Lys Arg	



65		70		75		80
Ala Glu Tyr	Ala Ile Pro Phe Ala Thr	Gly Cys Met Gly His Cys His				
	85	90	95			
Tyr Cys Tyr	Leu Gln Thr Thr Met Gly Ser Lys Pro Tyr Ile Arg Thr					
	100	105	110			
Tyr Val Asn Val	Glu Glu Ile Leu Glu Gln Ala Asp Gln Tyr Ile Lys					
	115	120	125			
Glu Arg Ala Pro	Glu Asp Thr Arg Phe Glu Ala Ser Cys Thr Ser Asp					
	130	135	140			
Ile Val Gly Ile	Asp His Leu Thr His Thr Leu Lys Arg Ala Ile Glu					
	145	150	155			160
His Phe Gly Gln	Thr Asp His Gly Lys Leu Arg Phe Val Thr Lys Phe					
	165	170	175			
His His Val Asp	His Leu Leu Asp Ala Lys His Asn Gly Lys Thr Arg					
	180	185	190			
Phe Arg Phe Ser	Val Asn Ala Glu Tyr Val Ile Lys Ser Phe Glu Pro					
	195	200	205			
Gly Thr Ser Pro	Leu Asp Lys Arg Ile Glu Ala Ala Val Lys Val Ala					
	210	215	220			
Glu Ala Gly Tyr	Pro Leu Gly Phe Ile Ile Ala Pro Ile Tyr Ile His					
	225	230	235			240
Asp Gly Trp Gln	Glu Gly Tyr Arg Val Leu Leu Glu Lys Leu Asp Arg					
	245	250	255			
Ala Leu Pro Gln	His Ala Arg Arg Asp Ile Thr Phe Glu Met Ile Gln					
	260	265	270			
His Arg Phe Thr	Lys Pro Ala Lys Arg Val Ile Glu Lys Asn Tyr Pro					
	275	280	285			
Lys Thr Lys Leu	Glu Leu Asp Glu Glu Lys Arg Arg Tyr Lys Trp Gly					
	290	295	300			

Arg Tyr Gly Ile Gly Lys Tyr Ile Tyr Gln Lys Asp Glu Glu Ala Glu  
 305 310 315 320

Leu Arg Ser Ala Leu Glu Ser Tyr Ile Asp Asn Tyr Phe Pro Glu Ala  
 325 330 335

Lys Ile Glu Tyr Phe Thr  
 340

<210> 41  
 <211> 905  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(905)

<400> 41  
 acaataacag tacaggccgg gaagacggga tatacaaggc ttgcaaagcg gacgctcgtc 60  
 tccatttcat cgaaagacgg aaccgatttg atcgccgtca caatcaatgc ccctgacgac 120  
 tggaatgatc atatgaacat gttcaactat gtattcggcc agtacaaaac atatatcatc 180  
 gccaaaaaag gcgagattcc gaaattaaaa gactcttttt acggacatac agcttttatt 240  
 aaacgggatg tcacatatct tttaaacgaa gaggaaaaag aagatgtgaa ggttgatatc 300  
 gagcttcttg aaccgaaaaa atcatggcgt aaaaacaaaa aagaaatccc ggacatcatc 360  
 ggagaaatga acgtcatggt cgacggaaaa acgattgcaa gcgtaccgat ctattatgaa 420  
 aacgagcgaa acaaaaatcc gaaaaaatcg tttttcgaga cttttcaatc cgtattccaa 480  
 aaagcggcgg gcggttcatc atg gtc aat ata atc tgg gtc ggc tta acg gtg 533  
 Met Val Asn Ile Ile Trp Val Gly Leu Thr Val  
 1 5 10  
 atc ggt atg gtg ttt gcg ctt ttc aac ggc acg gtt cag gaa gtt aat 581  
 Ile Gly Met Val Phe Ala Leu Phe Asn Gly Thr Val Gln Glu Val Asn  
 15 20 25  
 gaa gct gta ttt aaa gga tcg aag gaa gcc gtc acg att gtg atc gga 629  
 Glu Ala Val Phe Lys Gly Ser Lys Glu Ala Val Thr Ile Val Ile Gly  
 30 35 40  
 ctg atg agc gtc ctt gtt ttt tgg ctg ggg gtg atg aaa atc gct gaa 677  
 Leu Met Ser Val Leu Val Phe Trp Leu Gly Val Met Lys Ile Ala Glu  
 45 50 55

cag tcc ggg ctt ctc gaa aaa ttc agc agg ctg tgc cgg ccg ttc att 725  
 Gln Ser Gly Leu Leu Glu Lys Phe Ser Arg Leu Cys Arg Pro Phe Ile  
 60 65 70 75

tcg aag ctg ttt ccc gag atc cct ccg gat cat ccg gcg atg gga tat 773  
 Ser Lys Leu Phe Pro Glu Ile Pro Pro Asp His Pro Ala Met Gly Tyr  
 80 85 90

att tta tcc aat tta atg gcc aac ttt ttc gga ttg ggc aat gca gcg 821  
 Ile Leu Ser Asn Leu Met Ala Asn Phe Phe Gly Leu Gly Asn Ala Ala  
 95 100 105

aca ccg ctc ggt att aaa gcg atg gaa cag atg aag gcg ctc aac ccg 869  
 Thr Pro Leu Gly Ile Lys Ala Met Glu Gln Met Lys Ala Leu Asn Arg  
 110 115 120

aac cgc agg gaa gcg agc cgc tca atg cac cca ggc 905  
 Asn Arg Arg Glu Ala Ser Arg Ser Met His Pro Gly  
 125 130 135

<210> 42  
 <211> 135  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 42

Met Val Asn Ile Ile Trp Val Gly Leu Thr Val Ile Gly Met Val Phe  
 1 5 10 15

Ala Leu Phe Asn Gly Thr Val Gln Glu Val Asn Glu Ala Val Phe Lys  
 20 25 30

Gly Ser Lys Glu Ala Val Thr Ile Val Ile Gly Leu Met Ser Val Leu  
 35 40 45

Val Phe Trp Leu Gly Val Met Lys Ile Ala Glu Gln Ser Gly Leu Leu  
 50 55 60

Glu Lys Phe Ser Arg Leu Cys Arg Pro Phe Ile Ser Lys Leu Phe Pro  
 65 70 75 80

Glu Ile Pro Pro Asp His Pro Ala Met Gly Tyr Ile Leu Ser Asn Leu  
 85 90 95

Met Ala Asn Phe Phe Gly Leu Gly Asn Ala Ala Thr Pro Leu Gly Ile  
 100 105 110

Lys Ala Met Glu Gln Met Lys Ala Leu Asn Arg Asn Arg Arg Glu Ala

115

120

125

Ser Arg Ser Met His Pro Gly  
130 135

<210> 43  
<211> 1568  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(1076)

<220>  
<221> CDS  
<222> (1112)..(1567)

<400> 43  
gattagatct tcagtttttt gcatctaaaa aaggagtagg ttcaacgaaa aacggacgtg 60  
actctgaagc gaagcgccta ggtgctaaac gtgcagacgg tcaattcgta tctggccggt 120  
caatccttta tcgtcagcgc ggaacaaaaa tctatccaag tgaaaacgtt gggcgcggcc 180  
gatattacac tctatttgca aaagtcgacg gaactgttaa attcgaacct ttcggccgta 240  
ccccaaaaa agtgagcgta tctcctgtag cctaaccttt aaacgaaact ccggtcgttc 300  
tgaccggagt tttttacatt cagcaccatg acttgcttaa aacaccttcc cgacgcctaa 360  
ataaggccgg gtttccgctc tgattctgct tcgttaaagt atataaacgt gtttcattta 420  
tactgccttc tctgttataa ttcaaagtac aaactgaatc agactcctaa aagagagacc 480  
aaacgattgg gagtgccaaa atg gaa gaa act tcg aaa aaa cga gaa aag aat 533  
Met Glu Glu Thr Ser Lys Lys Arg Glu Lys Asn  
1 5 10  
atg gac gat aag gct ttg acc cat gag ctt atc cat ctg ctc agc cac 581  
Met Asp Asp Lys Ala Leu Thr His Glu Leu Ile His Leu Leu Ser His  
15 20 25  
tca agg cac gac tgg atg aat aaa ctg caa ttg att aaa gga aac tta 629  
Ser Arg His Asp Trp Met Asn Lys Leu Gln Leu Ile Lys Gly Asn Leu  
30 35 40  
aca tta aaa aag tat gac cgc gta ttt gaa att atc gat gaa gtg gtc 677  
Thr Leu Lys Lys Tyr Asp Arg Val Phe Glu Ile Ile Asp Glu Val Val  
45 50 55  
atc gaa gct cag cat gaa tca aag ctt tca aac ctt aga atc ccg cgc 725  
Ile Glu Ala Gln His Glu Ser Lys Leu Ser Asn Leu Arg Ile Pro Arg  
60 65 70 75



gcg gcg tat gag ctg ctt aca ttt aac tgg atg gcc cat tcg ctg acg Ala Ala Tyr Glu Leu Leu Thr Phe Asn Trp Met Ala His Ser Leu Thr 80 85 90	773
ctt gaa tat gag gtg atc ggt caa gtc aag gat ttg tca gct tat gaa Leu Glu Tyr Glu Val Ile Gly Gln Val Lys Asp Leu Ser Ala Tyr Glu 95 100 105	821
gaa agg ctc gtc gtt ctc atc aga aag ctg ttt ggg att ttt gac gat Glu Arg Leu Val Val Leu Ile Arg Lys Leu Phe Gly Ile Phe Asp Asp 110 115 120	869
gcc gtt ttg aaa ggc agc gac aat cat ctg acg atc acg ctg cag acg Ala Val Leu Lys Gly Ser Asp Asn His Leu Thr Ile Thr Leu Gln Thr 125 130 135	917
gac ggt ccg gac gac cgc ctc gtc atc ttt ctc gat ttc cac ggc gta Asp Gly Pro Asp Asp Arg Leu Val Ile Phe Leu Asp Phe His Gly Val 140 145 150 155	965
ttc aca aag ctg acc ggt atc aaa gac ttt cat cat tca ctg gcc gac Phe Thr Lys Leu Thr Gly Ile Lys Asp Phe His His Ser Leu Ala Asp 160 165 170	1013
ttt tat gaa atc aag cgg ttt gat gta aca gac cgt gag tgc atc gcc Phe Tyr Glu Ile Lys Arg Phe Asp Val Thr Asp Arg Glu Cys Ile Ala 175 180 185	1061
gaa att cat atc aag taaagcgggtt ttttaggaat agaacggagg acatt atg Glu Ile His Ile Lys Met 190	1114
ttt gtt gat cag gtg aaa ata tac gta aaa ggc gga gac gga ggc aac Phe Val Asp Gln Val Lys Ile Tyr Val Lys Gly Gly Asp Gly Gly Asn 195 200 205	1162
ggt atg gtt gct ttc cgc cgc gaa aaa tat gtg cca aaa gga ggc cct Gly Met Val Ala Phe Arg Arg Glu Lys Tyr Val Pro Lys Gly Gly Pro 210 215 220 225	1210
gcc gga ggt gac ggc gga aaa ggc gga gac gtc gtt ttc aaa gtt gac Ala Gly Gly Asp Gly Gly Lys Gly Gly Asp Val Val Phe Lys Val Asp 230 235 240	1258
gaa ggt ctc agc acg ctg atg gat ttt aga tat caa aga cat ttt aag Glu Gly Leu Ser Thr Leu Met Asp Phe Arg Tyr Gln Arg His Phe Lys 245 250 255	1306
gca gcg cgc gga gaa cac ggc atg tct aaa aac cag cac ggc cga aat Ala Ala Arg Gly Glu His Gly Met Ser Lys Asn Gln His Gly Arg Asn 260 265 270	1354
gcc gaa gac atg gtt gtg aaa gtc ccg ccc ggc acg gtt gtc att gac Ala Glu Asp Met Val Val Lys Val Pro Pro Gly Thr Val Val Ile Asp 275 280 285	1402

gat gat aca aaa cag gtc atc gct gat tta acg gag cac gga cag gaa 1450  
 Asp Asp Thr Lys Gln Val Ile Ala Asp Leu Thr Glu His Gly Gln Glu  
 290 295 300 305

gcc gtc atc gca aaa ggg gga cgc ggc gga cgg ggc aat aca cgt ttt 1498  
 Ala Val Ile Ala Lys Gly Gly Arg Gly Gly Arg Gly Asn Thr Arg Phe  
 310 315 320

gcg acg cct gcc aac ccg gcg ccg cag ctt tct gaa aac ggc gaa ccc 1546  
 Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu Ser Glu Asn Gly Glu Pro  
 325 330 335

ggc aag gag cgc tat att gtt c 1568  
 Gly Lys Glu Arg Tyr Ile Val  
 340

<210> 44  
 <211> 192  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 44

Met Glu Glu Thr Ser Lys Lys Arg Glu Lys Asn Met Asp Asp Lys Ala  
 1 5 10 15

Leu Thr His Glu Leu Ile His Leu Leu Ser His Ser Arg His Asp Trp  
 20 25 30

Met Asn Lys Leu Gln Leu Ile Lys Gly Asn Leu Thr Leu Lys Lys Tyr  
 35 40 45

Asp Arg Val Phe Glu Ile Ile Asp Glu Val Val Ile Glu Ala Gln His  
 50 55 60

Glu Ser Lys Leu Ser Asn Leu Arg Ile Pro Arg Ala Ala Tyr Glu Leu  
 65 70 75 80

Leu Thr Phe Asn Trp Met Ala His Ser Leu Thr Leu Glu Tyr Glu Val  
 85 90 95

Ile Gly Gln Val Lys Asp Leu Ser Ala Tyr Glu Glu Arg Leu Val Val  
 100 105 110

Leu Ile Arg Lys Leu Phe Gly Ile Phe Asp Asp Ala Val Leu Lys Gly  
 115 120 125

Ser Asp Asn His Leu Thr Ile Thr Leu Gln Thr Asp Gly Pro Asp Asp

130                      135                      140  
 Arg Leu Val Ile Phe Leu Asp Phe His Gly Val Phe Thr Lys Leu Thr  
 145                      150                      155                      160  
  
 Gly Ile Lys Asp Phe His His Ser Leu Ala Asp Phe Tyr Glu Ile Lys  
                     165                      170                      175  
  
 Arg Phe Asp Val Thr Asp Arg Glu Cys Ile Ala Glu Ile His Ile Lys  
                     180                      185                      190  
  
 <210> 45  
 <211> 152  
 <212> PRT  
 <213> Bacillus licheniformis  
  
 <400> 45  
  
 Met Phe Val Asp Gln Val Lys Ile Tyr Val Lys Gly Gly Asp Gly Gly  
 1                      5                      10                      15  
  
 Asn Gly Met Val Ala Phe Arg Arg Glu Lys Tyr Val Pro Lys Gly Gly  
                     20                      25                      30  
  
 Pro Ala Gly Gly Asp Gly Gly Lys Gly Gly Asp Val Val Phe Lys Val  
                     35                      40                      45  
  
 Asp Glu Gly Leu Ser Thr Leu Met Asp Phe Arg Tyr Gln Arg His Phe  
 50                      55                      60  
  
 Lys Ala Ala Arg Gly Glu His Gly Met Ser Lys Asn Gln His Gly Arg  
 65                      70                      75                      80  
  
 Asn Ala Glu Asp Met Val Val Lys Val Pro Pro Gly Thr Val Val Ile  
                     85                      90                      95  
  
 Asp Asp Asp Thr Lys Gln Val Ile Ala Asp Leu Thr Glu His Gly Gln  
                     100                      105                      110  
  
 Glu Ala Val Ile Ala Lys Gly Gly Arg Gly Gly Arg Gly Asn Thr Arg  
                     115                      120                      125  
  
 Phe Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu Ser Glu Asn Gly Glu  
                     130                      135                      140

Pro Gly Lys Glu Arg Tyr Ile Val  
145 150

<210> 46  
<211> 1849  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(1346)

<400> 46  
tcctgcaacg atccagcttg cgggggcgga aattgaactt gttccgacca tctcccgaga 60  
agtccggctg aaaagggtt tggaatcggg caaacaaaac tatgatttca tgattattga 120  
ctgcccgcgc tcattagggc tgcttacaat caatgcgctt acggcttccg attccgctcg 180  
gattccgggtc cagtgcgagt attatgcgct ggaagggttg agccagctgc tcaactctgt 240  
ccggctcgtg caaaaacatt taaatacggg tctgatgatc gacggcgat tgctgacaat 300  
gcttgatgca agaacgaatt taggcataca ggatcatgaa gaagtgaaga agtacttccg 360  
cgataaagta tacaaaacgg ttatcccccg gaatgtccgg ctccagtgaag cgccgagtca 420  
tggaagccg atcattttat atgatccccg ttccagagga gcggaagtct atttagaatt 480  
agcaaaggaa gtggctgcga atg cct aaa ggt ctc gga aaa ggg att aat gca 533  
Met Pro Lys Gly Leu Gly Lys Gly Ile Asn Ala  
1 5 10  
ttg ttt tca aat gtt gat tta tcc gaa gaa acg gtt gag gaa atc aag 581  
Leu Phe Ser Asn Val Asp Leu Ser Glu Glu Thr Val Glu Glu Ile Lys  
15 20 25  
ctg caa gac ttg cgg ccc aac cct tat cag cca aga aaa acg ttt gat 629  
Leu Gln Asp Leu Arg Pro Asn Pro Tyr Gln Pro Arg Lys Thr Phe Asp  
30 35 40  
gac caa tcg tta aaa gat ttg aag gag tcc att ttg cag cac ggt gtt 677  
Asp Gln Ser Leu Lys Asp Leu Lys Glu Ser Ile Leu Gln His Gly Val  
45 50 55  
ttg cag ccc atc atc gtc aga aag tca att aaa ggc tat gac att gtg 725  
Leu Gln Pro Ile Ile Val Arg Lys Ser Ile Lys Gly Tyr Asp Ile Val  
60 65 70 75  
gcc gga gaa cgc cgt ttc cgg gct gct gaa aag gcc gga ttg gaa acc 773  
Ala Gly Glu Arg Arg Phe Arg Ala Ala Glu Lys Ala Gly Leu Glu Thr  
80 85 90  
att cct gcg att gtg cgc gag ctg tcg gaa tcc ctg atg atg gag att 821

Ile	Pro	Ala	Ile	Val	Arg	Glu	Leu	Ser	Glu	Ser	Leu	Met	Met	Glu	Ile		
			95					100					105				
gcc	cta	ttg	gaa	aat	ctt	caa	cga	gaa	gac	ctg	tct	ccg	ctt	gaa	gaa	869	
Ala	Leu	Leu	Glu	Asn	Leu	Gln	Arg	Glu	Asp	Leu	Ser	Pro	Leu	Glu	Glu		
		110					115					120					
gca	aaa	gcc	tat	gaa	tct	ttg	ctc	aaa	cat	ctc	gat	atg	acc	cag	gaa	917	
Ala	Lys	Ala	Tyr	Glu	Ser	Leu	Leu	Lys	His	Leu	Asp	Met	Thr	Gln	Glu		
		125					130				135						
cag	ctg	gcg	aaa	agg	ctt	gga	aaa	agc	agg	cct	cac	atc	gcc	aac	cac	965	
Gln	Leu	Ala	Lys	Arg	Leu	Gly	Lys	Ser	Arg	Pro	His	Ile	Ala	Asn	His		
140					145					150					155		
ttg	cgg	ctg	ctg	aca	ctt	cct	gaa	gac	gtt	caa	aag	tta	atc	gac	aac	1013	
Leu	Arg	Leu	Leu	Thr	Leu	Pro	Glu	Asp	Val	Gln	Lys	Leu	Ile	Asp	Asn		
				160					165					170			
ggc	acg	tta	tcg	atg	ggc	cat	ggc	cga	aca	ttg	ctt	gga	ttg	aaa	aac	1061	
Gly	Thr	Leu	Ser	Met	Gly	His	Gly	Arg	Thr	Leu	Leu	Gly	Leu	Lys	Asn		
			175					180					185				
aag	aaa	aag	ctt	gag	ccg	ctt	gtt	caa	aag	gtc	gtg	tcc	gaa	cag	ttg	1109	
Lys	Lys	Lys	Leu	Glu	Pro	Leu	Val	Gln	Lys	Val	Val	Ser	Glu	Gln	Leu		
		190					195					200					
aac	gtc	cgc	cag	ttg	gaa	aag	tta	att	caa	cag	ttg	aac	gct	gat	gtt	1157	
Asn	Val	Arg	Gln	Leu	Glu	Lys	Leu	Ile	Gln	Gln	Leu	Asn	Ala	Asp	Val		
	205						210				215						
cca	cgt	gaa	aca	aag	aag	ccg	aaa	caa	gtc	aaa	gat	gca	gtg	atc	aag	1205	
Pro	Arg	Glu	Thr	Lys	Lys	Pro	Lys	Gln	Val	Lys	Asp	Ala	Val	Ile	Lys		
220					225					230					235		
gaa	cgg	gaa	tcg	tat	ttg	cga	aac	tat	ttt	gga	aca	ccg	gtg	acc	att	1253	
Glu	Arg	Glu	Ser	Tyr	Leu	Arg	Asn	Tyr	Phe	Gly	Thr	Pro	Val	Thr	Ile		
				240					245					250			
aaa	aag	caa	aag	aaa	aaa	ggc	agg	atc	gaa	atc	gaa	ttc	tac	tca	aat	1301	
Lys	Lys	Gln	Lys	Lys	Lys	Gly	Arg	Ile	Glu	Ile	Glu	Phe	Tyr	Ser	Asn		
			255					260					265				
gaa	gac	ttg	gag	cgt	att	ctc	gaa	tta	ttg	gct	caa	gaa	gac	gca		1346	
Glu	Asp	Leu	Glu	Arg	Ile	Leu	Glu	Leu	Leu	Ala	Gln	Glu	Asp	Ala			
		270					275					280					
taagcttaaa	aaccatctga	tcacgtacag	atgggtttttt	tatgacattc	ttccggtcat											1406	
tcttttcaatt	ggtgacacat	ggcgccgctg	cgatccggtc	ttttccagat	gcgacagccc											1466	
gtccgcaagc	acatttgcca	tgctcatgac	aagattgagc	cttgtatttt	gcaggacaaa											1526	
atactccata	aaaccgctga	cattgacaat	tccgttaata	tgcacgtggc	cgacttccgg											1586	
caaacttttc	tgaacgcctg	ctccccgctt	caaaggccct	ttgccgattt	ggaaagaccc											1646	

cacgcttttg gttcgtccaa gacaggcgtc gatcgcgatc ataaaaggat tttgatgctg 1706  
 ctgatgaata tgatcaagct tttcatttaa gttcacggcg tgaaccgggt cggcaagcgt 1766  
 tccatagaca tgaaaacgtg tcagctgctt tgcggagagt ttcattccta cgagggggacc 1826  
 gagcgaatct ccggtcgagc ggt 1849

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 <212> PRT  
 <213> *Bacillus licheniformis*

<400> 47

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Asp Leu Ser Glu Glu Thr Val Glu Glu Ile Lys Leu Gln Asp Leu Arg  
 20 25 30

Pro Asn Pro Tyr Gln Pro Arg Lys Thr Phe Asp Asp Gln Ser Leu Lys  
 35 40 45

Asp Leu Lys Glu Ser Ile Leu Gln His Gly Val Leu Gln Pro Ile Ile  
 50 55 60

Val Arg Lys Ser Ile Lys Gly Tyr Asp Ile Val Ala Gly Glu Arg Arg  
 65 70 75 80

Phe Arg Ala Ala Glu Lys Ala Gly Leu Glu Thr Ile Pro Ala Ile Val  
 85 90 95

Arg Glu Leu Ser Glu Ser Leu Met Met Glu Ile Ala Leu Leu Glu Asn  
 100 105 110

Leu Gln Arg Glu Asp Leu Ser Pro Leu Glu Glu Ala Lys Ala Tyr Glu  
 115 120 125

Ser Leu Leu Lys His Leu Asp Met Thr Gln Glu Gln Leu Ala Lys Arg  
 130 135 140

Leu Gly Lys Ser Arg Pro His Ile Ala Asn His Leu Arg Leu Leu Thr  
 145 150 155 160

Leu Pro Glu Asp Val Gln Lys Leu Ile Asp Asn Gly Thr Leu Ser Met

165	170	175
Gly His Gly Arg Thr Leu Leu Gly Leu Lys Asn Lys Lys Lys Leu Glu		
180	185	190
Pro Leu Val Gln Lys Val Val Ser Glu Gln Leu Asn Val Arg Gln Leu		
195	200	205
Glu Lys Leu Ile Gln Gln Leu Asn Ala Asp Val Pro Arg Glu Thr Lys		
210	215	220
Lys Pro Lys Gln Val Lys Asp Ala Val Ile Lys Glu Arg Glu Ser Tyr		
225	230	235
Lys Pro Lys Gln Val Lys Asp Ala Val Ile Lys Glu Arg Glu Ser Tyr		
245	250	255
Lys Gly Arg Ile Glu Ile Glu Phe Tyr Ser Asn Glu Asp Leu Glu Arg		
260	265	270
Ile Leu Glu Leu Leu Ala Gln Glu Asp Ala		
275	280	

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 <212> DNA  
 <213> Bacillus licheniformis

<220>  
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 <222> (501)..(2987)

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agaaatcaac aacatggcgg tgtagctcag ctggctagag cgtacggttc ataccctga	180
ggtcgggggt tcgatccct cgcgcgtac ttatatgaag gcccgttggt caagtggta	240
agacaccgcc ctttcacggc ggtaacacgg gttcgaatcc cgtacgggtc attccggaaa	300
ccggcttctt ctgaagccgg ttttttgctg cataaaaaata tgcaaaaataa cgggaatgga	360
ctcgacttat caagagtgat tgaagcatgc taaaaaagc gtcgaacagt tctttgaatt	420
cgttaccttc ttttgacaaa atcctatttc atctttcgct ataattggcaa gcaacgaata	480

aacgagtggg agatgagagc atg gaa aaa gcg gaa aga aga gtg aac agc cca	533
Met Glu Lys Ala Glu Arg Arg Val Asn Ser Pro	
1 5 10	
ata gct gga cct gct gtt caa aaa ttg tat tca tgg ttt ggc agc atg	581
Ile Ala Gly Pro Ala Val Gln Lys Leu Tyr Ser Trp Phe Gly Ser Met	
15 20 25	
acg aag ctt atg atg cag cat tta tat tcc ctc ttt ttt tat aaa ggg	629
Thr Lys Leu Met Met Gln His Leu Tyr Ser Leu Phe Phe Tyr Lys Gly	
30 35 40	
ctg atc tat atg gtc atc ggt ttt tta ttg gga cga gcc ttc att ctg	677
Leu Ile Tyr Met Val Ile Gly Phe Leu Leu Gly Arg Ala Phe Ile Leu	
45 50 55	
tca gag gtc att ccc ttt gct ctt cca ttt ttc gga gcg atg ctt tta	725
Ser Glu Val Ile Pro Phe Ala Leu Pro Phe Phe Gly Ala Met Leu Leu	
60 65 70 75	
atc aaa aaa gat aaa gct ttc ctt gca tgc ctg gcg ctt ctt gcc gga	773
Ile Lys Lys Asp Lys Ala Phe Leu Ala Cys Leu Ala Leu Leu Ala Gly	
80 85 90	
gct ctg agc ata tcg cct cag cat tcg ctg ttc gtg ctt gcg gct ctg	821
Ala Leu Ser Ile Ser Pro Gln His Ser Leu Phe Val Leu Ala Ala Leu	
95 100 105	
ttt gca ttt gcg ata tgt tca aaa atg acg tcc ctt att ata aaa gac	869
Phe Ala Phe Ala Ile Cys Ser Lys Met Thr Ser Leu Ile Ile Lys Asp	
110 115 120	
cgt gtc aga acg ctg cct gtc gtc gtc ttt ttg gcg atg gct gtg aca	917
Arg Val Arg Thr Leu Pro Val Val Val Phe Leu Ala Met Ala Val Thr	
125 130 135	
aga tgc gga ttc gta tat gcc gaa tac gga acg gtt tca ggt tat cac	965
Arg Cys Gly Phe Val Tyr Ala Glu Tyr Gly Thr Val Ser Gly Tyr His	
140 145 150 155	
tat att atg gct ttc gtt gaa gcc gga tta tcg ttt atc ctc aca ttg	1013
Tyr Ile Met Ala Phe Val Glu Ala Gly Leu Ser Phe Ile Leu Thr Leu	
160 165 170	
att ttt ctg caa agc ctg ccg att gtc aca tca aag cgg gcg aaa cag	1061
Ile Phe Leu Gln Ser Leu Pro Ile Val Thr Ser Lys Arg Ala Lys Gln	
175 180 185	
tcg ctg aaa att gaa gag atc att tgt ttt atg att tta atc gct tcc	1109
Ser Leu Lys Ile Glu Glu Ile Ile Cys Phe Met Ile Leu Ile Ala Ser	
190 195 200	
gtt ctc acg ggc ttg aca ggc gtt tca ttt caa ggc atg cag gct gaa	1157
Val Leu Thr Gly Leu Thr Gly Val Ser Phe Gln Gly Met Gln Ala Glu	
205 210 215	



ctg ata ttg gcc cgt tat gtc gtg ctc gct ttc gcg ttc atc gga ggc Leu Ile Leu Ala Arg Tyr Val Val Leu Ala Phe Ala Phe Ile Gly Gly 220 225 230 235	1205
gca agc atc ggc tgt aca gtc ggg gtt gtg acc ggg ctg att ctc agc Ala Ser Ile Gly Cys Thr Val Gly Val Val Thr Gly Leu Ile Leu Ser 240 245 250	1253
ctc tca aac atc ggc aat tta tat cag atg agc ctg ctg gct ttc tca Leu Ser Asn Ile Gly Asn Leu Tyr Gln Met Ser Leu Leu Ala Phe Ser 255 260 265	1301
ggc ctt ctc ggc ggt ttg cta aaa gaa gga aaa aag ttc ggc gca gcg Gly Leu Leu Gly Gly Leu Leu Lys Glu Gly Lys Lys Phe Gly Ala Ala 270 275 280	1349
gtc ggc tta ttg att gga tct cta ttg att tct ctg tac gga gaa ggt Val Gly Leu Leu Ile Gly Ser Leu Leu Ile Ser Leu Tyr Gly Glu Gly 285 290 295	1397
tcg gct gaa tta gtg ccg acg ctt tat gaa tct ctg att gca atc ggc Ser Ala Glu Leu Val Pro Thr Leu Tyr Glu Ser Leu Ile Ala Ile Gly 300 305 310 315	1445
ctg ttc ctt tta acc cct cag tcg att acg aaa aaa gtg gcc aag tat Leu Phe Leu Leu Thr Pro Gln Ser Ile Thr Lys Lys Val Ala Lys Tyr 320 325 330	1493
ata cct gga acg act gag cac gcc cag gaa cag cag cag tat gca agg Ile Pro Gly Thr Lys Glu His Ala Gln Glu Gln Gln Tyr Ala Arg 335 340 345	1541
aaa atc cgc gat gtc acc gcc caa aaa gtc gat cag ttt tcg aac gtt Lys Ile Arg Asp Val Thr Ala Gln Lys Val Asp Gln Phe Ser Asn Val 350 355 360	1589
ttt cac gct tta tcc gaa agc ttc gct acc ttt tat cat tca gct ccg Phe His Ala Leu Ser Glu Ser Phe Ala Thr Phe Tyr His Ser Ala Pro 365 370 375	1637
gac gat gaa gga aaa gaa aaa gag atc gat ctg ttt ttg agc acg gtg Asp Asp Glu Gly Lys Glu Lys Glu Ile Asp Leu Phe Leu Ser Thr Val 380 385 390 395	1685
aca gaa cat tcc tgt cag tca tgc tat aag aaa aac aag tgc tgg gtt Thr Glu His Ser Cys Gln Ser Cys Tyr Lys Lys Asn Lys Cys Trp Val 400 405 410	1733
cag aac ttt gat aaa aca tat gat ttg atg aaa cgg gtt atg cag gaa Gln Asn Phe Asp Lys Thr Tyr Asp Leu Met Lys Arg Val Met Gln Glu 415 420 425	1781
acg gaa gaa aag caa tat ttt aaa aac cgc aag ctg aaa aag gag ttt Thr Glu Glu Lys Gln Tyr Phe Lys Asn Arg Lys Leu Lys Lys Glu Phe 430 435 440	1829
cat cag cac tgc tcc aaa tca aag caa gta gaa gcg ctg att gaa gac	1877

His	Gln	His	Cys	Ser	Lys	Ser	Lys	Gln	Val	Glu	Ala	Leu	Ile	Glu	Asp	
445						450					455					
gag	ctg	act	cat	ttt	agg	gcg	aac	cag	aca	tta	aaa	caa	aag	gtg	cat	1925
Glu	Leu	Thr	His	Phe	Arg	Ala	Asn	Gln	Thr	Leu	Lys	Gln	Lys	Val	His	
460					465					470					475	
gac	agc	aga	cgt	ctc	gtt	gca	gag	cag	ctt	ctc	ggc	gtt	tct	cag	gtt	1973
Asp	Ser	Arg	Arg	Leu	Val	Ala	Glu	Gln	Leu	Leu	Gly	Val	Ser	Gln	Val	
				480					485						490	
atg	gcg	gac	ttt	tct	cgg	gaa	ata	aaa	agg	gaa	agg	gag	cag	cat	ttt	2021
Met	Ala	Asp	Phe	Ser	Arg	Glu	Ile	Lys	Arg	Glu	Arg	Glu	Gln	His	Phe	
			495					500						505		
att	caa	gaa	gag	caa	att	cgg	gat	gcg	ctg	cag	cac	ttc	ggc	atc	gag	2069
Ile	Gln	Glu	Glu	Gln	Ile	Arg	Asp	Ala	Leu	Gln	His	Phe	Gly	Ile	Glu	
		510					515					520				
att	cag	caa	gtc	gaa	ata	tac	agc	ctt	gag	cag	gga	aac	atc	gat	att	2117
Ile	Gln	Gln	Val	Glu	Ile	Tyr	Ser	Leu	Glu	Gln	Gly	Asn	Ile	Asp	Ile	
	525					530					535					
gaa	atg	agt	atc	ccg	tat	tgc	aac	ggc	cat	gga	gag	tgt	gaa	aaa	atc	2165
Glu	Met	Ser	Ile	Pro	Tyr	Cys	Asn	Gly	His	Gly	Glu	Cys	Glu	Lys	Ile	
540					545					550					555	
atc	gct	ccg	atg	ctg	tcc	gat	att	ttg	gaa	gaa	caa	att	atc	gtc	aaa	2213
Ile	Ala	Pro	Met	Leu	Ser	Asp	Ile	Leu	Glu	Gln	Ile	Ile	Ile	Val	Lys	
				560					565						570	
gca	gaa	cag	tgc	gcc	ggc	cat	ccg	aat	gga	tat	tgt	cat	gtt	gcc	ttc	2261
Ala	Glu	Gln	Cys	Ala	Gly	His	Pro	Asn	Gly	Tyr	Cys	His	Val	Ala	Phe	
			575					580					585			
ggc	acc	ggc	aaa	tat	gcc	gcc	gcc	att	agc	gat	ggc	atg	gga	aat	ggc	2405
Gly	Thr	Gly	Lys	Tyr	Ala	Ala	Ala	Ile	Ser	Asp	Gly	Met	Gly	Asn	Gly	
620					625					630					635	
gca	agg	gcc	cat	ttt	gaa	agc	aat	gag	acg	atc	aag	ctg	ctg	gaa	aag	2453
Ala	Arg	Ala	His	Phe	Glu	Ser	Asn	Glu	Thr	Ile	Lys	Leu	Leu	Glu	Lys	
				640					645					650		
att	ctt	cag	tcg	ggc	atc	gac	gaa	aaa	gtg	gcg	att	aaa	acg	att	aac	2501
Ile	Leu	Gln	Ser	Gly	Ile	Asp	Glu	Lys	Val	Ala	Ile	Lys	Thr	Ile	Asn	
			655					660					665			
agc	att	ctt	tca	tta	agg	aca	aca	gat	gaa	att	tat	tcg	aca	ttg	gat	2549
Ser	Ile	Leu	Ser	Leu	Arg	Thr	Thr	Asp	Glu	Ile	Tyr	Ser	Thr	Leu	Asp	

670	675	680	
tta tcg gtc atc gat ctt cag gat gcg agc tgc aag ttt ttg aaa atc			2597
Leu Ser Val Ile Asp Leu Gln Asp Ala Ser Cys Lys Phe Leu Lys Ile			
685	690	695	
ggc tcc acc ccg agc ttt att aaa aga ggc gat caa att ata aaa gtg			2645
Gly Ser Thr Pro Ser Phe Ile Lys Arg Gly Asp Gln Ile Ile Lys Val			
700	705	710	715
cag gcc agc aat ctg ccg atc ggc atc att aca gaa ttc gat gtc gat			2693
Gln Ala Ser Asn Leu Pro Ile Gly Ile Ile Thr Glu Phe Asp Val Asp			
	720	725	730
gtt gtc agc gag caa tta aaa gcg gga gac ctt ttg atc atg atg agc			2741
Val Val Ser Glu Gln Leu Lys Ala Gly Asp Leu Leu Ile Met Met Ser			
	735	740	745
gac gga atc ttt gaa ggg ccg aga cat gtg gaa aat cat gat ctg tgg			2789
Asp Gly Ile Phe Glu Gly Pro Arg His Val Glu Asn His Asp Leu Trp			
	750	755	760
atg aag cgc aaa ttg aaa tcg ctg aaa acc gag gag ccg cag gaa atc			2837
Met Lys Arg Lys Leu Lys Ser Leu Lys Thr Glu Glu Pro Gln Glu Ile			
	765	770	775
gcc gac tta atc atg gaa gaa gtg atc cgg aca agg tcg ggt ctg att			2885
Ala Asp Leu Ile Met Glu Glu Val Ile Arg Thr Arg Ser Gly Leu Ile			
	780	785	790
gag gac gac atg acg gtg att gtc atc aag ctg gac cat aat acg cca			2933
Glu Asp Asp Met Thr Val Ile Val Ile Lys Leu Asp His Asn Thr Pro			
	800	805	810
aag tgg gcc tcc att ccg gcg ccg gct ttt ttc caa aag aat caa gag			2981
Lys Trp Ala Ser Ile Pro Ala Pro Ala Phe Phe Gln Lys Asn Gln Glu			
	815	820	825
att tct tagcattcgt ataaatcaaa tttcttctgg cgatgatgga actaaatcaa			3037
Ile Ser			
gatatctttg tccaggagga ataaaaacga tgaaaaaggg gcatttgaat caaatcctgc			3097
ttttgacgga cggtgtttca aaccgcggcg aagaccgcga ggccatggct gcctttgcga			3157
aagagcaggg aattaccgtg aatgtgattg ggattatgga cgagcatgaa atggatcagg			3217
aggcgatgaa agaagtcgaa gggatcgctc tcgcaggcgg aggagtccac caggtggttt			3277
acacgtcgca gctgtcgag accgttcaaa tgggtgacaaa aaaggcgatg acgcaaacc			3337
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aactgcctcc tgataaacgc ggtgaagtca tggaagtcgt tgacgagctt ggtgagaccg			3457
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 <213> Bacillus licheniformis

<400> 49

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 20 25 30

Gln His Leu Tyr Ser Leu Phe Phe Tyr Lys Gly Leu Ile Tyr Met Val  
 35 40 45

Ile Gly Phe Leu Leu Gly Arg Ala Phe Ile Leu Ser Glu Val Ile Pro  
 50 55 60

Phe Ala Leu Pro Phe Phe Gly Ala Met Leu Leu Ile Lys Lys Asp Lys  
 65 70 75 80

Ala Phe Leu Ala Cys Leu Ala Leu Leu Ala Gly Ala Leu Ser Ile Ser  
 85 90 95

Pro Gln His Ser Leu Phe Val Leu Ala Ala Leu Phe Ala Phe Ala Ile  
 100 105 110

Cys Ser Lys Met Thr Ser Leu Ile Ile Lys Asp Arg Val Arg Thr Leu  
 115 120 125

Pro Val Val Val Phe Leu Ala Met Ala Val Thr Arg Cys Gly Phe Val  
 130 135 140

Tyr Ala Glu Tyr Gly Thr Val Ser Gly Tyr His Tyr Ile Met Ala Phe  
 145 150 155 160

Val Glu Ala Gly Leu Ser Phe Ile Leu Thr Leu Ile Phe Leu Gln Ser  
 165 170 175

Leu Pro Ile Val Thr Ser Lys Arg Ala Lys Gln Ser Leu Lys Ile Glu  
 180 185 190

Glu Ile Ile Cys Phe Met Ile Leu Ile Ala Ser Val Leu Thr Gly Leu  
195 200 205

Thr Gly Val Ser Phe Gln Gly Met Gln Ala Glu Leu Ile Leu Ala Arg  
210 215 220

Tyr Val Val Leu Ala Phe Ala Phe Ile Gly Gly Ala Ser Ile Gly Cys  
225 230 235 240

Thr Val Gly Val Val Thr Gly Leu Ile Leu Ser Leu Ser Asn Ile Gly  
245 250 255

Asn Leu Tyr Gln Met Ser Leu Leu Ala Phe Ser Gly Leu Leu Gly Gly  
260 265 270

Leu Leu Lys Glu Gly Lys Lys Phe Gly Ala Ala Val Gly Leu Leu Ile  
275 280 285

Gly Ser Leu Leu Ile Ser Leu Tyr Gly Glu Gly Ser Ala Glu Leu Val  
290 295 300

Pro Thr Leu Tyr Glu Ser Leu Ile Ala Ile Gly Leu Phe Leu Leu Thr  
305 310 315 320

Pro Gln Ser Ile Thr Lys Lys Val Ala Lys Tyr Ile Pro Gly Thr Thr  
325 330 335

Glu His Ala Gln Glu Gln Gln Tyr Ala Arg Lys Ile Arg Asp Val  
340 345 350

Thr Ala Gln Lys Val Asp Gln Phe Ser Asn Val Phe His Ala Leu Ser  
355 360 365

Glu Ser Phe Ala Thr Phe Tyr His Ser Ala Pro Asp Asp Glu Gly Lys  
370 375 380

Glu Lys Glu Ile Asp Leu Phe Leu Ser Thr Val Thr Glu His Ser Cys  
385 390 395 400

Gln Ser Cys Tyr Lys Lys Asn Lys Cys Trp Val Gln Asn Phe Asp Lys  
405 410 415

Thr Tyr Asp Leu Met Lys Arg Val Met Gln Glu Thr Glu Glu Lys Gln

420	425	430
Tyr Phe Lys Asn Arg Lys Leu Lys Lys Glu Phe His Gln His Cys Ser		
435	440	445
Lys Ser Lys Gln Val Glu Ala Leu Ile Glu Asp Glu Leu Thr His Phe		
450	455	460
Arg Ala Asn Gln Thr Leu Lys Gln Lys Val His Asp Ser Arg Arg Leu		
465	470	475
Val Ala Glu Gln Leu Leu Gly Val Ser Gln Val Met Ala Asp Phe Ser		
485	490	495
Arg Glu Ile Lys Arg Glu Arg Glu Gln His Phe Ile Gln Glu Glu Gln		
500	505	510
Ile Arg Asp Ala Leu Gln His Phe Gly Ile Glu Ile Gln Gln Val Glu		
515	520	525
Ile Tyr Ser Leu Glu Gln Gly Asn Ile Asp Ile Glu Met Ser Ile Pro		
530	535	540
Tyr Cys Asn Gly His Gly Glu Cys Glu Lys Ile Ile Ala Pro Met Leu		
545	550	555
Ser Asp Ile Leu Glu Glu Gln Ile Ile Val Lys Ala Glu Gln Cys Ala		
565	570	575
Gly His Pro Asn Gly Tyr Cys His Val Ala Phe Gly Ser Ala Lys Ser		
580	585	590
Tyr Arg Val Val Thr Gly Ala Ala His Ala Ala Lys Gly Gly Gly Leu		
595	600	605
Val Ser Gly Asp Ser Tyr Asn Met Met Glu Leu Gly Thr Gly Lys Tyr		
610	615	620
Ala Ala Ala Ile Ser Asp Gly Met Gly Asn Gly Ala Arg Ala His Phe		
625	630	635
Glu Ser Asn Glu Thr Ile Lys Leu Leu Glu Lys Ile Leu Gln Ser Gly		
645	650	655

Ile Asp Glu Lys Val Ala Ile Lys Thr Ile Asn Ser Ile Leu Ser Leu  
660 665 670

Arg Thr Thr Asp Glu Ile Tyr Ser Thr Leu Asp Leu Ser Val Ile Asp  
675 680 685

Leu Gln Asp Ala Ser Cys Lys Phe Leu Lys Ile Gly Ser Thr Pro Ser  
690 695 700

Phe Ile Lys Arg Gly Asp Gln Ile Ile Lys Val Gln Ala Ser Asn Leu  
705 710 715 720

Pro Ile Gly Ile Ile Thr Glu Phe Asp Val Asp Val Val Ser Glu Gln  
725 730 735

Leu Lys Ala Gly Asp Leu Leu Ile Met Met Ser Asp Gly Ile Phe Glu  
740 745 750

Gly Pro Arg His Val Glu Asn His Asp Leu Trp Met Lys Arg Lys Leu  
755 760 765

Lys Ser Leu Lys Thr Glu Glu Pro Gln Glu Ile Ala Asp Leu Ile Met  
770 775 780

Glu Glu Val Ile Arg Thr Arg Ser Gly Leu Ile Glu Asp Asp Met Thr  
785 790 795 800

Val Ile Val Ile Lys Leu Asp His Asn Thr Pro Lys Trp Ala Ser Ile  
805 810 815

Pro Ala Pro Ala Phe Phe Gln Lys Asn Gln Glu Ile Ser  
820 825

<210> 50  
<211> 1928  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(1427)

<400> 50

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gagtttgaaa gcgccgctga tttggatgct gtctttgtga tcagaatgcc gctgaccaat	120
ttcaaaaccg ctgccccaaa cgtaacggag ctgccgatca gagaagtctc aaaaggaaaa	180
tatgaaggat attggaccgc tactttcaact gcaaaagcaa aaggagcggg aatcgaggtc	240
atcgtcagag atgattacgg caatgaaacg agacaaacgg caaaaggcaa gctgtatatc	300
aatgaaaagc tgaataaaag gtgaaaagac gctgtcttta atggcagcgt ttttttcggt	360
ttacgatcga caaattcagt acgaaaactt caaaaaatgt acgatttacg caacattaat	420
tgacagactt tacctttggg cttgatttat acttaggaaa acaaacacta aggtcaccga	480
gccgcagaaa ggggaaggat gtg gaa atc tat tta gat gcg ata tgg ctg tta	533
Val Glu Ile Tyr Leu Asp Ala Ile Trp Leu Leu	
1 5 10	
aac ttt tgt ttt gac ttg ctg ctt tta atg atg acc gca ttt att tta	581
Asn Phe Cys Phe Asp Leu Leu Leu Leu Met Met Thr Ala Phe Ile Leu	
15 20 25	
aag cga agg gtt aaa aag cgg agg ctg atc cta ggg gca ttt gtc gcg	629
Lys Arg Arg Val Lys Lys Arg Arg Leu Ile Leu Gly Ala Phe Val Ala	
30 35 40	
tca agc atc gtt ctg ttt atg ttt aca cct ttt tca ccg tac gtc ctt	677
Ser Ser Ile Val Leu Phe Met Phe Thr Pro Phe Ser Pro Tyr Val Leu	
45 50 55	
cat cct gcc ggc aaa ctg tcg ttt tcg gtt gtg atc gtt ctt gtg gca	725
His Pro Ala Gly Lys Leu Ser Phe Ser Val Val Ile Val Leu Val Ala	
60 65 70 75	
ttt ggt ttt aag cgg ttc cgg ttt ttt ttg cag aat ttg ttt tct ttt	773
Phe Gly Phe Lys Arg Phe Arg Phe Phe Leu Gln Asn Leu Phe Ser Phe	
80 85 90	
tat ttt gcc act ttt tta atg gga gga ggg att atc gga gcg cat tct	821
Tyr Phe Ala Thr Phe Leu Met Gly Gly Gly Ile Ile Gly Ala His Ser	
95 100 105	
ttg ctt gaa acg gat tcg atc atg gaa aac ggc gtc ttt atg acg aat	869
Leu Leu Glu Thr Asp Ser Ile Met Glu Asn Gly Val Phe Met Thr Asn	
110 115 120	
tgg tcc ggt ttt gga gac ccc gtc agc tgg ctg ttt gtc tgt gtg ggt	917
Trp Ser Gly Phe Gly Asp Pro Val Ser Trp Leu Phe Val Cys Val Gly	
125 130 135	
ttt gcg gct gta tgg ctg ttt tca aaa aag cgt ttt gaa gat gct gaa	965
Phe Ala Ala Val Trp Leu Phe Ser Lys Lys Arg Phe Glu Asp Ala Glu	
140 145 150 155	
gcg aag aaa att caa tac gaa gaa cgc gtc cgc cta gag gcc tgc att	1013



Ala Lys Lys Ile Gln Tyr Glu Glu Arg Val Arg Leu Glu Ala Cys Ile	
160 165 170	
ggt gaa cat acg ctt cat ttc acc gga ttg att gac tcc gga aac cag	1061
Gly Glu His Thr Leu His Phe Thr Gly Leu Ile Asp Ser Gly Asn Gln	
175 180 185	
ctc tac gat cca atc aca aaa acg ccc gtc atg atc gtc aat att gaa	1109
Leu Tyr Asp Pro Ile Thr Lys Thr Pro Val Met Ile Val Asn Ile Glu	
190 195 200	
aaa ttg aaa gtt gta ttg gga gaa gag gca agt gtg acc atc aag gaa	1157
Lys Leu Lys Val Val Leu Gly Glu Glu Ala Ser Val Thr Ile Lys Glu	
205 210 215	
atg agc ccg ctt gat gcc gtc ggg aaa ctg gat gaa gca ctg ccg tat	1205
Met Ser Pro Leu Asp Ala Val Gly Lys Leu Asp Glu Ala Leu Pro Tyr	
220 225 230 235	
atc ggg cgg atc cgc ctg att ccg tac cgc ggg gtc ggc cat cag cat	1253
Ile Gly Arg Ile Arg Leu Ile Pro Tyr Arg Gly Val Gly His Gln His	
240 245 250	
cag ttt ctg ctc tgc tta aag ccg gat cat gtg ctc gtt tgt acg gaa	1301
Gln Phe Leu Leu Cys Leu Lys Pro Asp His Val Leu Val Cys Thr Glu	
255 260 265	
aga gaa gtg att gaa gcg ccg aaa tgc ctg att ggc atc agc aca tca	1349
Arg Glu Val Ile Glu Ala Pro Lys Cys Leu Ile Gly Ile Ser Thr Ser	
270 275 280	
ccg ctt tcc gct gac ggc gaa ttt gac gcc atc gtc cat ccg aaa atg	1397
Pro Leu Ser Ala Asp Gly Glu Phe Asp Ala Ile Val His Pro Lys Met	
285 290 295	
ctg gcc gga aac ccg gtc aaa cac gtt tct taaacttgaa gtctgttaca	1447
Leu Ala Gly Asn Pro Val Lys His Val Ser	
300 305	
ttatcatact cctgaagacg tttattttaga agggggagga agatgaaaaa actaaaatta	1507
aggttaacct atctatggta caaactttta atgaaactgg ggctgaaaag cgacgaaatt	1567
tattatatcg gcggaagcga ggcgcttccc ccgccattgt caaaagatga agagcagggtg	1627
cttctccata agctgcctga cggtgatcag gcggcacgag cgattttgat tgaacgaaat	1687
ctcagactgg tcgtgtacat cgcgagaaaa tttgaaaata caggaatcaa tatcgaggat	1747
ttaatctcca tcggcacgat cgggctcatc aaagcgggtga atacgtttta tcccagagaaa	1807
aaaatcaaac tggttacata tgcttccaga tgcattgaaa atgaaatttt gatgtattta	1867
agaagaaaca ataaaatccg ttcagaggta tcattcgacg aaccgctgaa catcgattgg	1927
g	1928

<210> 51  
 <211> 309  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 51

Val Glu Ile Tyr Leu Asp Ala Ile Trp Leu Leu Asn Phe Cys Phe Asp  
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Leu Leu Leu Leu Met Met Thr Ala Phe Ile Leu Lys Arg Arg Val Lys  
 20 25 30

Lys Arg Arg Leu Ile Leu Gly Ala Phe Val Ala Ser Ser Ile Val Leu  
 35 40 45

Phe Met Phe Thr Pro Phe Ser Pro Tyr Val Leu His Pro Ala Gly Lys  
 50 55 60

Leu Ser Phe Ser Val Val Ile Val Leu Val Ala Phe Gly Phe Lys Arg  
 65 70 75 80

Phe Arg Phe Phe Leu Gln Asn Leu Phe Ser Phe Tyr Phe Ala Thr Phe  
 85 90 95

Leu Met Gly Gly Gly Ile Ile Gly Ala His Ser Leu Leu Glu Thr Asp  
 100 105 110

Ser Ile Met Glu Asn Gly Val Phe Met Thr Asn Trp Ser Gly Phe Gly  
 115 120 125

Asp Pro Val Ser Trp Leu Phe Val Cys Val Gly Phe Ala Ala Val Trp  
 130 135 140

Leu Phe Ser Lys Lys Arg Phe Glu Asp Ala Glu Ala Lys Lys Ile Gln  
 145 150 155 160

Tyr Glu Glu Arg Val Arg Leu Glu Ala Cys Ile Gly Glu His Thr Leu  
 165 170 175

His Phe Thr Gly Leu Ile Asp Ser Gly Asn Gln Leu Tyr Asp Pro Ile  
 180 185 190

Thr Lys Thr Pro Val Met Ile Val Asn Ile Glu Lys Leu Lys Val Val

195	200	205
Leu Gly Glu Glu Ala Ser Val Thr Ile Lys Glu Met Ser Pro Leu Asp 210	215	220
Ala Val Gly Lys Leu Asp Glu Ala Leu Pro Tyr Ile Gly Arg Ile Arg 225	230	235 240
Leu Ile Pro Tyr Arg Gly Val Gly His Gln His Gln Phe Leu Leu Cys 245	250	255
Leu Lys Pro Asp His Val Leu Val Cys Thr Glu Arg Glu Val Ile Glu 260	265	270
Ala Pro Lys Cys Leu Ile Gly Ile Ser Thr Ser Pro Leu Ser Ala Asp 275	280	285
Gly Glu Phe Asp Ala Ile Val His Pro Lys Met Leu Ala Gly Asn Pro 290	295	300
Val Lys His Val Ser 305		

<210> 52  
 <211> 1922  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1421)

<400> 52	
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taagatcatg aagctttttct ttggacaagt caatccgacg gttttgacaa tggcggcggtt	180
aagggtggtg tcatctttga tcgaactgac ggcggctgtt gtgatgcttt tgacaaacga	240
cgtcagaaaa gctgtggcgg tcaacagcgt actggccatg gtcgggccgc tcatctttat	300
tattacaatg acaatcggca tctatcagat tgcagggcag ctttcttacg caaagctgat	360
tttgatcttt atgggagtgg ttttgatcat cgcggggatc tataaatagc gacacatgat	420
aagagaggcc gacttgtcat aatgtcttcc tttgatcata catttttata gaagacaagc	480

aaaaagagga gggagtgttt ttg cac cac atc aca gag att ctc ccc gat acg	533
Leu His His Ile Thr Glu Ile Leu Pro Asp Thr	
1 5 10	
atc aaa cgc gcg ctc agc ggt ctt ggc gac cat gaa atc gat cag ata	581
Ile Lys Arg Ala Leu Ser Gly Leu Gly Asp His Glu Ile Asp Gln Ile	
15 20 25	
gaa gaa att cgg gtt cgg aca agt cgt ccg ctg gaa ctg gtg aac aaa	629
Glu Glu Ile Arg Val Arg Thr Ser Arg Pro Leu Glu Leu Val Asn Lys	
30 35 40	
gga aag ccg cgc ttt ctc cct tat gtg gcg acg cct gaa gac tcg gcg	677
Gly Lys Pro Arg Phe Leu Pro Tyr Val Ala Thr Pro Glu Asp Ser Ala	
45 50 55	
ctt ctt tta aac aga ttg gga aat tac agc atg tat aca ctg gaa gag	725
Leu Leu Leu Asn Arg Leu Gly Asn Tyr Ser Met Tyr Thr Leu Glu Glu	
60 65 70 75	
gaa ttg aaa aaa gga tat gtc acg atc aga ggc gga cac cgc gtg ggg	773
Glu Leu Lys Lys Gly Tyr Val Thr Ile Arg Gly Gly His Arg Val Gly	
80 85 90	
ctt gcc ggc cgg gtt gtc gtc gaa aac ggg gcc gtc aaa gga atc aga	821
Leu Ala Gly Arg Val Val Val Glu Asn Gly Ala Val Lys Gly Ile Arg	
95 100 105	
gaa ata tca tca ttt aat att cgc att gcc aaa gaa aaa atc ggc att	869
Glu Ile Ser Ser Phe Asn Ile Arg Ile Ala Lys Glu Lys Ile Gly Ile	
110 115 120	
tcc aaa ccg tat gtc ccc cat tta ttt caa aac tcg tgg ctg aac acg	917
Ser Lys Pro Tyr Val Pro His Leu Phe Gln Asn Ser Trp Leu Asn Thr	
125 130 135	
ctg att atc ggt ccg ccg caa acc gga aaa aca aca ctg ctc aga gac	965
Leu Ile Ile Gly Pro Pro Gln Thr Gly Lys Thr Thr Leu Leu Arg Asp	
140 145 150 155	
ctc gcc agg ctg atc agt tcg gga agc ggc aac gcc cct gcc aaa aaa	1013
Leu Ala Arg Leu Ile Ser Ser Gly Ser Gly Asn Ala Pro Ala Lys Lys	
160 165 170	
gtg ggg att gtt gac gaa agg tct gaa atc gca ggc tgt gta aac ggc	1061
Val Gly Ile Val Asp Glu Arg Ser Glu Ile Ala Gly Cys Val Asn Gly	
175 180 185	
ata ccg caa tat cgg ctc ggc gac cgg gca gac atc ctt gac gcc tgt	1109
Ile Pro Gln Tyr Arg Leu Gly Asp Arg Ala Asp Ile Leu Asp Ala Cys	
190 195 200	
cca aaa gcg gaa ggg ctg atg atg atg atc aga tcg atg agt ccg gag	1157
Pro Lys Ala Glu Gly Leu Met Met Met Ile Arg Ser Met Ser Pro Glu	
205 210 215	

gta atg atc gcc gat gag atc ggg aga atg gaa gac gca gaa gcg ctc	1205
Val Met Ile Ala Asp Glu Ile Gly Arg Met Glu Asp Ala Glu Ala Leu	
220 225 230 235	
ttg gaa gcg gtc cac gcg ggg gtg act gtc atc gtt tcg gct cac ggc	1253
Leu Glu Ala Val His Ala Gly Val Thr Val Ile Val Ser Ala His Gly	
240 245 250	
tac aca tat gca gat ctc gcc agg cgt cca tca ttg aaa atg ctt caa	1301
Tyr Thr Tyr Ala Asp Leu Ala Arg Arg Pro Ser Leu Lys Met Leu Gln	
255 260 265	
gag cac cgg gtt ttt gag cga atc gtg gaa ctt tcc aga aag aac ggt	1349
Glu His Arg Val Phe Glu Arg Ile Val Glu Leu Ser Arg Lys Asn Gly	
270 275 280	
ccc ggc agc ctg agc cgc atc cta aat ggg aac gga gag ccg ctc ggg	1397
Pro Gly Ser Leu Ser Arg Ile Leu Asn Gly Asn Gly Glu Pro Leu Gly	
285 290 295	
gca gca aag agg atg tta tca tgc tgaagctttt aggtgccgtg cttatttttg	1451
Ala Ala Lys Arg Met Leu Ser Cys	
300 305	
cagcagccac atggacagga tttgaaatgg cgaagccttt cagggaaagg ccgaagcaaa	1511
tccgccagct gttggccgct ttgcagtctt tggaggctga aatcatgtac gggcatacac	1571
cgctccgtca ggcatacaaaa cagatcgcac accagcttac cgagccggta gcctctttgt	1631
ttcagacatt tgcagaacag cttgaaaaag gcagcgcttc agcagggacg gcatgggaag	1691
acagcctgga gaaagtatgg cccgaaacgg ctcttaaaaa gaaagaatac gagattttac	1751
ggcaattcgg cgaaacgctg ggccgctcatg atctgatttc tcagcaaaaa catatcaaac	1811
tggcgtaaac ccatttagag acagaggaag ctgaagcaaa tctcgcccag gcgaaaaatg	1871
aaaaaatggt caaaagcctt ggatttttga cgggactgct actgattctt c	1922

<210> 53  
 <211> 307  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 53

Leu His His Ile Thr Glu Ile Leu Pro Asp Thr Ile Lys Arg Ala Leu
1 5 10 15

Ser Gly Leu Gly Asp His Glu Ile Asp Gln Ile Glu Glu Ile Arg Val
20 25 30

Arg Thr Ser Arg Pro Leu Glu Leu Val Asn Lys Gly Lys Pro Arg Phe

35	40	45
Leu Pro Tyr Val Ala Thr	Pro Glu Asp Ser Ala	Leu Leu Leu Asn Arg
50	55	60
Leu Gly Asn Tyr Ser Met Tyr Thr	Leu Glu Glu Glu Leu Lys Lys Gly	
65	70	75 80
Tyr Val Thr Ile Arg Gly Gly His Arg	Val Gly Leu Ala Gly Arg Val	
85	90	95
Val Val Glu Asn Gly Ala Val Lys Gly Ile Arg Glu Ile Ser Ser Phe		
100	105	110
Asn Ile Arg Ile Ala Lys Glu Lys Ile Gly Ile Ser Lys Pro Tyr Val		
115	120	125
Pro His Leu Phe Gln Asn Ser Trp Leu Asn Thr Leu Ile Ile Gly Pro		
130	135	140
Pro Gln Thr Gly Lys Thr Thr Leu Leu Arg Asp Leu Ala Arg Leu Ile		
145	150	155 160
Ser Ser Gly Ser Gly Asn Ala Pro Ala Lys Lys Val Gly Ile Val Asp		
165	170	175
Glu Arg Ser Glu Ile Ala Gly Cys Val Asn Gly Ile Pro Gln Tyr Arg		
180	185	190
Leu Gly Asp Arg Ala Asp Ile Leu Asp Ala Cys Pro Lys Ala Glu Gly		
195	200	205
Leu Met Met Met Ile Arg Ser Met Ser Pro Glu Val Met Ile Ala Asp		
210	215	220
Glu Ile Gly Arg Met Glu Asp Ala Glu Ala Leu Leu Glu Ala Val His		
225	230	235 240
Ala Gly Val Thr Val Ile Val Ser Ala His Gly Tyr Thr Tyr Ala Asp		
245	250	255
Leu Ala Arg Arg Pro Ser Leu Lys Met Leu Gln Glu His Arg Val Phe		
260	265	270

Glu Arg Ile Val Glu Leu Ser Arg Lys Asn Gly Pro Gly Ser Leu Ser  
 275 280 285

Arg Ile Leu Asn Gly Asn Gly Glu Pro Leu Gly Ala Ala Lys Arg Met  
 290 295 300

Leu Ser Cys  
 305

<210> 54  
 <211> 1511  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (498)..(1010)

<220>  
 <221> CDS  
 <222> (1036)..(1239)

<220>  
 <221> CDS  
 <222> (1255)..(1509)

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 atcgcaggct gtgtaaacgg cataccgcaa tatcggctcg gcgaccgggc agacatcctt 180  
 gacgcctgtc caaaagcggg agggctgatg atgatgatca gatcgatgag tccggaggta 240  
 atgatcgccg atgagatcgg gagaatggaa gacgcagaag cgctcttgga agcgggtccac 300  
 gcgggggtga ctgtcatcgt ttcggctcac ggctacacat atgcagatct cgccaggcgt 360  
 ccatcattga aaatgcttca agagcaccgg gtttttgagc gaatcgtgga actttccaga 420  
 aagaacgggtc ccggcagcct gagccgcata ctaaattggga acggagagcc gctcggggca 480  
 gcaaagagga tggtatc atg ctg aag ctt tta ggt gcc gtg ctt att ttg 530  
 Met Leu Lys Leu Leu Gly Ala Val Leu Ile Leu  
 1 5 10  
 gca gca gcc aca tgg aca gga ttt gaa atg gcg aag cct ttc agg gaa 578  
 Ala Ala Ala Thr Trp Thr Gly Phe Glu Met Ala Lys Pro Phe Arg Glu  
 15 20 25

agg ccg aag caa atc cgc cag ctg ttg gcc gct ttg cag tct ttg gag	626
Arg Pro Lys Gln Ile Arg Gln Leu Leu Ala Ala Leu Gln Ser Leu Glu	
30 35 40	
gct gaa atc atg tac ggg cat aca ccg ctc cgt cag gca tca aaa cag	674
Ala Glu Ile Met Tyr Gly His Thr Pro Leu Arg Gln Ala Ser Lys Gln	
45 50 55	
atc gca cac cag ctt acc gag ccg gta gcc tct ttg ttt cag aca ttt	722
Ile Ala His Gln Leu Thr Glu Pro Val Ala Ser Leu Phe Gln Thr Phe	
60 65 70 75	
gca gaa cag ctt gaa aaa ggc agc gct tca gca ggg acg gca tgg gaa	770
Ala Glu Gln Leu Glu Lys Gly Ser Ala Ser Ala Gly Thr Ala Trp Glu	
80 85 90	
gac agc ctg gag aaa gta tgg ccc gaa acg gct ctt aaa aag aaa gaa	818
Asp Ser Leu Glu Lys Val Trp Pro Glu Thr Ala Leu Lys Lys Lys Glu	
95 100 105	
tac gag att tta cgg caa ttc ggc gaa acg ctg ggc cgt cat gat ctg	866
Tyr Glu Ile Leu Arg Gln Phe Gly Glu Thr Leu Gly Arg His Asp Leu	
110 115 120	
att tct cag caa aaa cat atc aaa ctg gcg tta acc cat tta gag aca	914
Ile Ser Gln Gln Lys His Ile Lys Leu Ala Leu Thr His Leu Glu Thr	
125 130 135	
gag gaa gct gaa gca aat ctc gcc cag gcg aaa aat gaa aaa atg gtc	962
Glu Glu Ala Glu Ala Asn Leu Ala Gln Ala Lys Asn Glu Lys Met Val	
140 145 150 155	
aaa agc ctt gga ttt ttg acg gga ctg cta ctg att ctt cta ttg atg	1010
Lys Ser Leu Gly Phe Leu Thr Gly Leu Leu Leu Ile Leu Leu Leu Met	
160 165 170	
taatgaagag gggagcatac acgaa atg gga gta gac gta aat att att ttt	1062
Met Gly Val Asp Val Asn Ile Ile Phe	
175 180	
caa att gcc ggc gtc ggg atc gtc gtc gct ttt ctt cac acc ata ctg	1110
Gln Ile Ala Gly Val Gly Ile Val Val Ala Phe Leu His Thr Ile Leu	
185 190 195	
gat caa atg ggg aag aag gaa tat gcc caa tgg gtc acg ctt tta gga	1158
Asp Gln Met Gly Lys Lys Glu Tyr Ala Gln Trp Val Thr Leu Leu Gly	
200 205 210	
ttc att tat ata ttg ttc atg gtg gca act gtt gtc gat gat cta ttc	1206
Phe Ile Tyr Ile Leu Phe Met Val Ala Thr Val Val Asp Asp Leu Phe	
215 220 225	
caa aag ata aaa gct gtc ttt cta ttt caa gga taggggggct cactc att	1257
Gln Lys Ile Lys Ala Val Phe Leu Phe Gln Gly Ile	
230 235 240	
gaa atc gtt caa atc gta gga ctg gga atg atc gcc acc ttc ctc agc	1305



Glu Ile Val Gln Ile Val Gly Leu Gly Met Ile Ala Thr Phe Leu Ser	
245 250 255	
ttg att gtg aaa gag caa aaa ccg acg ttt gct ttt ttg att gtc gtt	1353
Leu Ile Val Lys Glu Gln Lys Pro Thr Phe Ala Phe Leu Ile Val Val	
260 265 270	
ttt gcc ggc tgc acg att ttt tta ttc tta gta gat cag gtc tac gaa	1401
Phe Ala Gly Cys Thr Ile Phe Leu Phe Leu Val Asp Gln Val Tyr Glu	
275 280 285	
atc att cgg atg att gaa aaa ata gct gcc aat gcc aac atc aac atg	1449
Ile Ile Arg Met Ile Glu Lys Ile Ala Ala Asn Ala Asn Ile Asn Met	
290 295 300	
atg tat gtc gaa acg att ttg aag att atc ggg att gct tat att gcg	1497
Met Tyr Val Glu Thr Ile Leu Lys Ile Ile Gly Ile Ala Tyr Ile Ala	
305 310 315 320	
gag ttt ggc gcc ca	1511
Glu Phe Gly Ala	

<210> 55  
 <211> 171  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 55

Met Leu Lys Leu Leu Gly Ala Val Leu Ile Leu Ala Ala Ala Thr Trp
1 5 10 15

Thr Gly Phe Glu Met Ala Lys Pro Phe Arg Glu Arg Pro Lys Gln Ile
20 25 30

Arg Gln Leu Leu Ala Ala Leu Gln Ser Leu Glu Ala Glu Ile Met Tyr
35 40 45

Gly His Thr Pro Leu Arg Gln Ala Ser Lys Gln Ile Ala His Gln Leu
50 55 60

Thr Glu Pro Val Ala Ser Leu Phe Gln Thr Phe Ala Glu Gln Leu Glu
65 70 75 80

Lys Gly Ser Ala Ser Ala Gly Thr Ala Trp Glu Asp Ser Leu Glu Lys
85 90 95

Val Trp Pro Glu Thr Ala Leu Lys Lys Lys Glu Tyr Glu Ile Leu Arg
100 105 110

Gln Phe Gly Glu Thr Leu Gly Arg His Asp Leu Ile Ser Gln Gln Lys  
 115 120 125

His Ile Lys Leu Ala Leu Thr His Leu Glu Thr Glu Glu Ala Glu Ala  
 130 135 140

Asn Leu Ala Gln Ala Lys Asn Glu Lys Met Val Lys Ser Leu Gly Phe  
 145 150 155 160

Leu Thr Gly Leu Leu Leu Ile Leu Leu Leu Met  
 165 170

<210> 56  
 <211> 68  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 56

Met Gly Val Asp Val Asn Ile Ile Phe Gln Ile Ala Gly Val Gly Ile  
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Val Val Ala Phe Leu His Thr Ile Leu Asp Gln Met Gly Lys Lys Glu  
 20 25 30

Tyr Ala Gln Trp Val Thr Leu Leu Gly Phe Ile Tyr Ile Leu Phe Met  
 35 40 45

Val Ala Thr Val Val Asp Asp Leu Phe Gln Lys Ile Lys Ala Val Phe  
 50 55 60

Leu Phe Gln Gly  
 65

<210> 57  
 <211> 85  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 57

Ile Glu Ile Val Gln Ile Val Gly Leu Gly Met Ile Ala Thr Phe Leu  
 1 5 10 15

Ser Leu Ile Val Lys Glu Gln Lys Pro Thr Phe Ala Phe Leu Ile Val

20

25

30

Val Phe Ala Gly Cys Thr Ile Phe Leu Phe Leu Val Asp Gln Val Tyr  
 35 40 45

Glu Ile Ile Arg Met Ile Glu Lys Ile Ala Ala Asn Ala Asn Ile Asn  
 50 55 60

Met Met Tyr Val Glu Thr Ile Leu Lys Ile Ile Gly Ile Ala Tyr Ile  
 65 70 75 80

Ala Glu Phe Gly Ala  
 85

&lt;210&gt; 58

&lt;211&gt; 1207

&lt;212&gt; DNA

&lt;213&gt; Bacillus licheniformis

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (501)..(704)

&lt;400&gt; 58

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ccagctgttg gccgctttgc agtctttgga ggctgaaatc atgtacgggc atacaccgct 120

ccgtcaggca tcaaaacaga tcgcacacca gcttaccgag ccggtagcct ctttgtttca 180

gacatttgca gaacagcttg aaaaaggcag cgcttcagca gggacggcat gggaagacag 240

cctggagaaa gtatggcccg aaacggctct taaaaagaaa gaatacgaga ttttacggca 300

attcggcgaa acgctgggccc gtcattgatct gattttctcag caaaaacata tcaaactggc 360

gttaacccat ttagagacag aggaagctga agcaaattct gcccaggcga aaaatgaaaa 420

aatggtcaaa agccttgat ttttgacggg actgctactg attcttctat tgatgtaatg 480

aagaggggag catacacgaa atg gga gta gac gta aat att att ttt caa att 533

Met Gly Val Asp Val Asn Ile Ile Phe Gln Ile  
 1 5 10

gcc ggc gtc ggg atc gtc gtc gct ttt ctt cac acc ata ctg gat caa 581

Ala Gly Val Gly Ile Val Val Ala Phe Leu His Thr Ile Leu Asp Gln  
 15 20 25

atg ggg aag aag gaa tat gcc caa tgg gtc acg ctt tta gga ttc att 629

Met Gly Lys Lys Glu Tyr Ala Gln Trp Val Thr Leu Leu Gly Phe Ile  
 30 35 40

tat ata ttg ttc atg gtg gca act gtt gtc gat gat cta ttc caa aag	677
Tyr Ile Leu Phe Met Val Ala Thr Val Val Asp Asp Leu Phe Gln Lys	
45 50 55	

ata aaa gct gtc ttt cta ttt caa gga taggggggct cactcattga	724
Ile Lys Ala Val Phe Leu Phe Gln Gly	
60 65	

aatcgttcaa atcgtaggac tgggaatgat cgccaccttc ctcagcttga ttgtgaaaga	784
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gcaaaaaccg acgtttgctt ttttgattgt cgtttttgcc ggctgcacga tttttttatt	844
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cttagtagat caggtctacg aaatcattcg gatgattgaa aaaatagctg ccaatgccaa	904
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catcaacatg atgtatgtcg aaacgatttt gaagattatc gggattgctt atattgcgga	964
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gtttggcgcc cagctgacaa aggatgccgg acaggggtgcg attgcttcga agatcgaatt	1024
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ggcaggcaaa atcctcatct tagtcatggc tgtgcctatt ttaaccgtga ttatcgaaac	1084
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gatcatcgga ctcatccctt ccatgtctta gtcagaaagg aggatttcct gagtgaagcg	1144
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ttttctgttc tggctcttgg tcatcggaat cgtatgcttt ggagcgcata atgtacaagc	1204
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ttc	1207
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<211> 68

<212> PRT

<213> Bacillus licheniformis

<400> 59

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20 25 30

Tyr Ala Gln Trp Val Thr Leu Leu Gly Phe Ile Tyr Ile Leu Phe Met
35 40 45

Val Ala Thr Val Val Asp Asp Leu Phe Gln Lys Ile Lys Ala Val Phe
50 55 60

Leu Phe Gln Gly
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<211> 2153

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<220>  
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 <222> (501)..(1703)

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ccaccttcct cagcttgatt gtgaaagagc aaaaaccgac gtttgctttt ttgattgtcg      180

tttttgccgg ctgcacgatt tttttattct tagtagatca ggtctacgaa atcattcgga      240

tgattgaaaa aatagctgcc aatgccaca tcaacatgat gtatgtcgaa acgattttga      300

agattatcgg gattgcttat attgcggagt ttggcgccca gctgacaaaag gatgccggac      360

aggggtgcgat tgcttcgaag atcgaattgg caggcaaaat cctcatctta gtcattggctg      420

tgcctatttt aaccgtgatt atcgaaacga tcatcggact catcccttcc atgtcttagt      480

cagaaaggag gatttcctga gtg aag cgt ttt ctg ttc tgg ctc ttg gtc atc      533
                Val Lys Arg Phe Leu Phe Trp Leu Leu Val Ile
                  1             5             10

gga atc gta tgc ttt gga gcg cat aat gta caa gct tcg cca aaa gaa      581
Gly Ile Val Cys Phe Gly Ala His Asn Val Gln Ala Ser Pro Lys Glu
                15             20             25

gcg gag ccg gct ggg gaa acc gct gca gaa gaa tcg gca gaa gcc att      629
Ala Glu Pro Ala Gly Glu Thr Ala Ala Glu Glu Ser Ala Glu Ala Ile
                30             35             40

gca aga gag cag gct gaa ggt ttg gaa cta gac cgg gtc ggg gag ttc      677
Ala Arg Glu Gln Ala Glu Gly Leu Glu Leu Asp Arg Val Gly Glu Phe
                45             50             55

tgg aac aac att ttg aca gag tat ggg gga cac ctt ccc gaa agt caa      725
Trp Asn Asn Ile Leu Thr Glu Tyr Gly Gly His Leu Pro Glu Ser Gln
                60             65             70             75

aaa gga agc ctg ctt gaa ttt gtc aaa gga gaa aag cac ttt tcg cct      773
Lys Gly Ser Leu Leu Glu Phe Val Lys Gly Glu Lys His Phe Ser Pro
                80             85             90

gag gaa tgg ggc aaa gcg ctg ttt tcc tac ttg ttc cat gaa gtg ctg      821
Glu Glu Trp Gly Lys Ala Leu Phe Ser Tyr Leu Phe His Glu Val Leu
                95             100             105

gct aac ggg aaa ctg ctg ggg acg ctg atc ctg ttg acc atc ttc tgc      869
Ala Asn Gly Lys Leu Leu Gly Thr Leu Ile Leu Leu Thr Ile Phe Cys
                110             115             120

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gtc ctg ctt cag ctt ttg caa aac gcg ttt caa caa agc acc gtc agc Val Leu Leu Gln Leu Leu Gln Asn Ala Phe Gln Gln Ser Thr Val Ser 125 130 135	917
aaa gtg gcg tat gca att gtc tac atg gtg ctg att att ctt gcg ctc Lys Val Ala Tyr Ala Ile Val Tyr Met Val Leu Ile Ile Leu Ala Leu 140 145 150 155	965
aac agc ttt cgg gtt gcc gtc aca tat gcg aat gaa gcg att cag acg Asn Ser Phe Arg Val Ala Val Thr Tyr Ala Asn Glu Ala Ile Gln Thr 160 165 170	1013
atg aca agc ttt atc ctg tcg ctc gta cct ctg ctt ctg gcg ctg atg Met Thr Ser Phe Ile Leu Ser Leu Val Pro Leu Leu Leu Ala Leu Met 175 180 185	1061
gcg act tcg ggg gga gcc gcc tca gcc gca ttc ttt cat ccg gtc att Ala Thr Ser Gly Gly Ala Ala Ser Ala Ala Phe Phe His Pro Val Ile 190 195 200	1109
ctt ttt ctc atg aac acg agc ggc ttg ttt atc caa tat atc gtg ttg Leu Phe Leu Met Asn Thr Ser Gly Leu Phe Ile Gln Tyr Ile Val Leu 205 210 215	1157
ccg ctt tta ttt tta tca gcg att tta agc att gtc agc acg atg acg Pro Leu Leu Phe Leu Ser Ala Ile Leu Ser Ile Val Ser Thr Met Thr 220 225 230 235	1205
gac caa tat aaa gtc aca cag ctg gcc cag ctc ctc aga aat gcg gcg Asp Gln Tyr Lys Val Thr Gln Leu Ala Gln Leu Leu Arg Asn Ala Ala 240 245 250	1253
atc ggc acg ctg gct gca ttt ttg acc gta ttc ctc ggt gtc atc tcg Ile Gly Thr Leu Ala Ala Phe Leu Thr Val Phe Leu Gly Val Ile Ser 255 260 265	1301
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gca aaa ttc att acc gga aac ttc atc ccc gta ttg ggc cgc atg ttt Ala Lys Phe Ile Thr Gly Asn Phe Ile Pro Val Leu Gly Arg Met Phe 285 290 295	1397
acc gaa gcg aca gac acg gtg atc agc gcg tct ctc ctg ctg aaa aac Thr Glu Ala Thr Asp Thr Val Ile Ser Ala Ser Leu Leu Leu Lys Asn 300 305 310 315	1445
acc gtc ggg ata ctc ggt gtg gca atc tta att tgc atc gca gcc ttt Thr Val Gly Ile Leu Gly Val Ala Ile Leu Ile Cys Ile Ala Ala Phe 320 325 330	1493
ccc gcg atc aaa atc ctt tcc ctc gcg ctc ata tac aaa att gcc gcg Pro Ala Ile Lys Ile Leu Ser Leu Ala Leu Ile Tyr Lys Ile Ala Ala 335 340 345	1541
gcg gtt ctc cag cct ctc gga ggc ggc ccg gtt atc agc tgc ctg gat	1589

Ala Val Leu Gln Pro Leu Gly Gly Gly Pro Val Ile Ser Cys Leu Asp	
350 355 360	
gtc atc agc aaa agc gtc atc tac att ttc gcg gcc atg gcc atc gtt	1637
Val Ile Ser Lys Ser Val Ile Tyr Ile Phe Ala Ala Met Ala Ile Val	
365 370 375	
tcg ctg atg ttt ttc tta agc tta acc gtg atc att aca gcg ggg aat	1685
Ser Leu Met Phe Phe Leu Ser Leu Thr Val Ile Ile Thr Ala Gly Asn	
380 385 390 395	
ctg acg atg atg atg aag tagggaggga tgagatggaa tttctgacag	1733
Leu Thr Met Met Met Lys	
400	
agtggctcac gaatattatt ctatttattc tgatggcgat cgtcatcgat atgcttctgc	1793
cgaattcgag catgcaaaaa tacgcgaaaa tggatgatcag cctgctcttg atcgttgtaa	1853
tactgaaccc gatcttctct ttattcagga cagatccgga tgtgattttt gagaagctta	1913
caaaaaacgg acaagttcag tcaaacgaaa taaaaaatca gctgaattca gaaaaaaaaag	1973
aaatacaagc ctcacaacaa gcatatatct tagaacagat ggctgttcaa ttggaaaaga	2033
acgcagaggg caggtttaca agcgacaaat acaagataga ccgagtcgag gtctcttctg	2093
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Glu Thr Ala Ala Glu Glu Ser Ala Glu Ala Ile Ala Arg Glu Gln Ala	
35 40 45	
Glu Gly Leu Glu Leu Asp Arg Val Gly Glu Phe Trp Asn Asn Ile Leu	
50 55 60	
Thr Glu Tyr Gly Gly His Leu Pro Glu Ser Gln Lys Gly Ser Leu Leu	
65 70 75 80	

Glu Phe Val Lys Gly Glu Lys His Phe Ser Pro Glu Glu Trp Gly Lys  
85 90 95

Ala Leu Phe Ser Tyr Leu Phe His Glu Val Leu Ala Asn Gly Lys Leu  
100 105 110

Leu Gly Thr Leu Ile Leu Leu Thr Ile Phe Cys Val Leu Leu Gln Leu  
115 120 125

Leu Gln Asn Ala Phe Gln Gln Ser Thr Val Ser Lys Val Ala Tyr Ala  
130 135 140

Ile Val Tyr Met Val Leu Ile Ile Leu Ala Leu Asn Ser Phe Arg Val  
145 150 155 160

Ala Val Thr Tyr Ala Asn Glu Ala Ile Gln Thr Met Thr Ser Phe Ile  
165 170 175

Leu Ser Leu Val Pro Leu Leu Leu Ala Leu Met Ala Thr Ser Gly Gly  
180 185 190

Ala Ala Ser Ala Ala Phe Phe His Pro Val Ile Leu Phe Leu Met Asn  
195 200 205

Thr Ser Gly Leu Phe Ile Gln Tyr Ile Val Leu Pro Leu Leu Phe Leu  
210 215 220

Ser Ala Ile Leu Ser Ile Val Ser Thr Met Thr Asp Gln Tyr Lys Val  
225 230 235 240

Thr Gln Leu Ala Gln Leu Leu Arg Asn Ala Ala Ile Gly Thr Leu Ala  
245 250 255

Ala Phe Leu Thr Val Phe Leu Gly Val Ile Ser Val Gln Gly Ala Ser  
260 265 270

Ala Ala Val Thr Asp Gly Ile Thr Leu Arg Thr Ala Lys Phe Ile Thr  
275 280 285

Gly Asn Phe Ile Pro Val Leu Gly Arg Met Phe Thr Glu Ala Thr Asp  
290 295 300

Thr Val Ile Ser Ala Ser Leu Leu Leu Lys Asn Thr Val Gly Ile Leu



305 310 315 320

Gly Val Ala Ile Leu Ile Cys Ile Ala Ala Phe Pro Ala Ile Lys Ile  
325 330 335

Leu Ser Leu Ala Leu Ile Tyr Lys Ile Ala Ala Ala Val Leu Gln Pro  
340 345 350

Leu Gly Gly Gly Pro Val Ile Ser Cys Leu Asp Val Ile Ser Lys Ser  
355 360 365

Val Ile Tyr Ile Phe Ala Ala Met Ala Ile Val Ser Leu Met Phe Phe  
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ttcagaaaaa aaagaaatac aagcctcaca acaagcatat atcttagaac agatggctgt 180  
tcaattggaa aagaacgcag agggcaggtt tacaagcgac aaatacaaga tagaccgagt 240  
cgaggtctct tctgacagcc agctgaaaac agagaaagac ctgagtaagc atgcggaagt 300  
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caatacggac cggagctacc agtccatgca ggaaagagaa aagaaagaga cgggggaagt 420  
cagagaacag ctagcaggca tctgggaaat aagccccgac aagattacag ttcatatcga 480  
aggggggagaa cgaagcggca atg aat aaa aga acc tgg atc gaa aag ctg atc 533  
Met Asn Lys Arg Thr Trp Ile Glu Lys Leu Ile  
1 5 10

ggc cac ctg ctc ccg aaa gac gag aaa gac gga aaa aag ctg acg aaa	581
Gly His Leu Leu Pro Lys Asp Glu Lys Asp Gly Lys Lys Leu Thr Lys	
15 20 25	
tat cac tac ttt ctg ctg ctt ttt gtt ctc ggc gtt tcc ttc atg ctc	629
Tyr His Tyr Phe Leu Leu Leu Phe Val Leu Gly Val Ser Phe Met Leu	
30 35 40	
gtc agc cag atc ttc tct tcc gaa cct tcc caa gag cca gcg gca gat	677
Val Ser Gln Ile Phe Ser Ser Glu Pro Ser Gln Glu Pro Ala Ala Asp	
45 50 55	
cag ccg gcg gct tca caa aaa gct acg tct gaa agc acc gta cag agc	725
Gln Pro Ala Ala Ser Gln Lys Ala Thr Ser Glu Ser Thr Val Gln Ser	
60 65 70 75	
ggg gaa gga gaa aaa gaa gtg ttc aag ccc gcc tca gat gac aaa ccg	773
Gly Glu Gly Glu Lys Glu Val Phe Lys Pro Ala Ser Asp Asp Lys Pro	
80 85 90	
aag gaa tcg atc caa gat tac gaa cag gaa tat gaa aat cag ctc aaa	821
Lys Glu Ser Ile Gln Asp Tyr Glu Gln Glu Tyr Glu Asn Gln Leu Lys	
95 100 105	
gac ata ttg gaa acc atc atc ggc gtt gag gac gtg tca atc gtc gtc	869
Asp Ile Leu Glu Thr Ile Ile Gly Val Glu Asp Val Ser Ile Val Val	
110 115 120	
aat gtt gat gca acc tca ttg aaa ata ttc gag aaa aac aga aaa acc	917
Asn Val Asp Ala Thr Ser Leu Lys Ile Phe Glu Lys Asn Arg Lys Thr	
125 130 135	
cag gaa act tca acg aat gag aca gat aaa cag gga ggc aag cgg acg	965
Gln Glu Thr Ser Thr Asn Glu Thr Asp Lys Gln Gly Gly Lys Arg Thr	
140 145 150 155	
gtg tct gaa atg tct tca gac gaa gaa atc gtc atc atc aaa aac gga	1013
Val Ser Glu Met Ser Ser Asp Glu Glu Ile Val Ile Ile Lys Asn Gly	
160 165 170	
gat aaa gag acg cct gtc gtc gtt cag acg aaa aag ccc gat atc agg	1061
Asp Lys Glu Thr Pro Val Val Val Gln Thr Lys Lys Pro Asp Ile Arg	
175 180 185	
ggg gtt ctc gtt gtc gct cag gga gtc gac aac gtt caa ata aaa aag	1109
Gly Val Leu Val Val Ala Gln Gly Val Asp Asn Val Gln Ile Lys Lys	
190 195 200	
acc att att gaa gca gtg aca agg gtt ctt gat gtt ccg agc cac cgc	1157
Thr Ile Ile Glu Ala Val Thr Arg Val Leu Asp Val Pro Ser His Arg	
205 210 215	
gtc gct gtt gcc cct aaa aaa atg aag gag gat tca taaatgatgc	1203
Val Ala Val Ala Pro Lys Lys Met Lys Glu Asp Ser	
220 225 230	

tgaaaaaaca aacggtttgg cttttaacca tgttaagtct cgtcgttgta ctgagtgtct 1263  
 actacattat gtcgcccgaag gagaaaaatg tcgtcacggt tgatgacaag gaacaagttg 1323  
 ccgctgaaaa agaaaaaccg atgaaagaag agcctgccaa ggatggcaaa gatgataccg 1383  
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 accgcatgga aatggacgat cagcgcagca gggagaggga ggaattaacc gaaatcgtca 1563  
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<400> 63

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Leu Leu Phe Val Leu Gly Val Ser Phe Met Leu Val Ser Gln Ile Phe  
 35 40 45

Ser Ser Glu Pro Ser Gln Glu Pro Ala Ala Asp Gln Pro Ala Ala Ser  
 50 55 60

Gln Lys Ala Thr Ser Glu Ser Thr Val Gln Ser Gly Glu Gly Glu Lys  
 65 70 75 80

Glu Val Phe Lys Pro Ala Ser Asp Asp Lys Pro Lys Glu Ser Ile Gln  
 85 90 95

Asp Tyr Glu Gln Glu Tyr Glu Asn Gln Leu Lys Asp Ile Leu Glu Thr  
 100 105 110

Ile Ile Gly Val Glu Asp Val Ser Ile Val Val Asn Val Asp Ala Thr  
 115 120 125

Ser Leu Lys Ile Phe Glu Lys Asn Arg Lys Thr Gln Glu Thr Ser Thr  
 130 135 140

Asn Glu Thr Asp Lys Gln Gly Gly Lys Arg Thr Val Ser Glu Met Ser  
 145 150 155 160

Ser Asp Glu Glu Ile Val Ile Ile Lys Asn Gly Asp Lys Glu Thr Pro  
 165 170 175

Val Val Val Gln Thr Lys Lys Pro Asp Ile Arg Gly Val Leu Val Val  
 180 185 190

Ala Gln Gly Val Asp Asn Val Gln Ile Lys Lys Thr Ile Ile Glu Ala  
 195 200 205

Val Thr Arg Val Leu Asp Val Pro Ser His Arg Val Ala Val Ala Pro  
 210 215 220

Lys Lys Met Lys Glu Asp Ser  
 225 230

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 <211> 1062  
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 aagacatatt ggaaaccatc atcggcggtg aggacgtgtc aatcgtcgtc aatgttgatg 180  
 caacctcatt gaaaatattc gagaaaaaca gaaaaaccca ggaaacttca acgaatgaga 240  
 cagataaaca gggaggcaag cggacgggtg ctgaaatgtc ttcagacgaa gaaatcgtca 300  
 tcatcaaaaa cggagataaa gagacgcctg tcgtcgttca gacgaaaaag cccgatatca 360  
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 aagcagtgac aagggttctt gatgttccga gccaccgcgt cgctgttgcc cctaaaaaaa 480  
 tgaaggagga ttcataa atg atg ctg aaa aaa caa acg gtt tgg ctt tta 530

	Met	Met	Leu	Lys	Lys	Gln	Thr	Val	Trp	Leu	Leu	
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acc atg tta agt ctc gtc gtt gta ctg agt gtc tac tac att atg tcg												578
Thr Met Leu Ser Leu Val Val Val Leu Ser Val Tyr Tyr Ile Met Ser												
			15				20			25		
ccc gaa gga gaa aat gtc gtc acg gtt gat gac aag gaa caa gtt gcc												626
Pro Glu Gly Glu Asn Val Val Thr Val Asp Asp Lys Glu Gln Val Ala												
		30				35			40			
gct gaa aaa gaa aaa ccg atg aaa gaa gag cct gcc aag gat ggc aaa												674
Ala Glu Lys Glu Lys Pro Met Lys Glu Glu Pro Ala Lys Asp Gly Lys												
	45				50			55				
gat gat acc gcg cct gct aaa gac aaa act aaa ggg aaa gat aca aaa												722
Asp Asp Thr Ala Pro Ala Lys Asp Lys Thr Lys Gly Lys Asp Thr Lys												
	60			65			70				75	
gat aaa gaa acg tct gcg agt gag cag aac gga gag gtt gtc aca gag												770
Asp Lys Glu Thr Ser Ala Ser Glu Gln Asn Gly Glu Val Val Thr Glu												
			80			85				90		
gaa tca tcg ggt gat gaa gat tta ttc aca aca tac cgc atg gaa atg												818
Glu Ser Ser Gly Asp Glu Asp Leu Phe Thr Thr Tyr Arg Met Glu Met												
		95				100			105			
gac gat cag cgc agc agg gag agg gag gaa tta acc gaa atc gtc aga												866
Asp Asp Gln Arg Ser Arg Glu Arg Glu Glu Leu Thr Glu Ile Val Arg												
		110			115			120				
agc gat aaa gcg acg gca aaa gaa aaa agc gaa gct tac gac aag atg												914
Ser Asp Lys Ala Thr Ala Lys Glu Lys Ser Glu Ala Tyr Asp Lys Met												
	125			130			135					
aca gag ctc agc gaa gct gaa gga acg gaa aag acc ctt gaa acc ctc												962
Thr Glu Leu Ser Glu Ala Glu Gly Thr Glu Lys Thr Leu Glu Thr Leu												
	140			145			150			155		
atc aaa aca aaa ggc tat taagacgcct tgggtcaacgc cgacggcgat												1010
Ile Lys Thr Lys Gly Tyr												
			160									
aaagtcaata ttacgggtgaa ggccaaggag cactcgaaag ccgcctgcac cg												1062
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Val Val Thr Val Asp Asp Lys Glu Gln Val Ala Ala Glu Lys Glu Lys  
 35 40 45

Pro Met Lys Glu Glu Pro Ala Lys Asp Gly Lys Asp Asp Thr Ala Pro  
 50 55 60

Ala Lys Asp Lys Thr Lys Gly Lys Asp Thr Lys Asp Lys Glu Thr Ser  
 65 70 75 80

Ala Ser Glu Gln Asn Gly Glu Val Val Thr Glu Glu Ser Ser Gly Asp  
 85 90 95

Glu Asp Leu Phe Thr Thr Tyr Arg Met Glu Met Asp Asp Gln Arg Ser  
 100 105 110

Arg Glu Arg Glu Glu Leu Thr Glu Ile Val Arg Ser Asp Lys Ala Thr  
 115 120 125

Ala Lys Glu Lys Ser Glu Ala Tyr Asp Lys Met Thr Glu Leu Ser Glu  
 130 135 140

Ala Glu Gly Thr Glu Lys Thr Leu Glu Thr Leu Ile Lys Thr Lys Gly  
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Tyr

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 <212> DNA  
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 <222> (501)..(2843)

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 aatataatcg aacaaaacaa ggacgcacag gaagagataa tccaatgatt ctgtataaaa 180

aaatgccgca ggaaatcgtg ttcgcagggc aggcggaaaa ctcgaactta aaacagatcg	240
atgtaaacag cgtaccactt ttagtcgaga tgaacggaga ggaagcaagg aacgttcaga	300
gttctcagca cgaacccgat ggatttttta aaacaagaaa cggcccctgg gcagacgctt	360
aaactgacat tttataaata gctggagtggt ctcaaggata aatatgctat aataggggaa	420
tccagaggaa aatcgcagcc gaaaaaaggc tgctttctct ttgtttttac attttttaac	480
acgcagtaag gtgatggaac atg gca aaa aga aaa cga aaa tca aca aag aaa	533
Met Ala Lys Arg Lys Arg Lys Ser Thr Lys Lys	
1 5 10	
caa aaa caa gga aaa aaa cgg atc cat ctt aaa ttt gaa ttg tac gga	581
Gln Lys Gln Gly Lys Lys Arg Ile His Leu Lys Phe Glu Leu Tyr Gly	
15 20 25	
tta atc tgt atc gcc atc tcg att att gcg gtt ttg cag ctt ggc gta	629
Leu Ile Cys Ile Ala Ile Ser Ile Ile Ala Val Leu Gln Leu Gly Val	
30 35 40	
gca ggg caa acg ttc att tac atg ttc cgc ttt ttc gcc ggt gaa tgg	677
Ala Gly Gln Thr Phe Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp	
45 50 55	
ttc atc ctt tgc ctt ctc ggc ctc ttt tta acg ggc ttg tct tta ttt	725
Phe Ile Leu Cys Leu Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe	
60 65 70 75	
tgg aaa aag aaa aca ccc agt ttt ttg acg agg aga aaa gcg ggc ctt	773
Trp Lys Lys Lys Thr Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu	
80 85 90	
tac tgc atc att gca agc atg ctg ctt ctt tca cat gtc cag ctg ttt	821
Tyr Cys Ile Ile Ala Ser Met Leu Leu Leu Ser His Val Gln Leu Phe	
95 100 105	
cag cat ttg acc gaa agg gga atg gtt cag tct ccg agc gtg atc caa	869
Gln His Leu Thr Glu Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln	
110 115 120	
aat acg tgg gag ctg ttt ctg atg gat gta aaa ggc gag aca gga tcg	917
Asn Thr Trp Glu Leu Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser	
125 130 135	
cct gat ctt gga ggc gga atg att gga gcc ctt tta ttc gcg gcg tca	965
Pro Asp Leu Gly Gly Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser	
140 145 150 155	
tat ttt ctg ttt gca tct gca gga tct aaa atc atc gcc gtc ttc ctg	1013
Tyr Phe Leu Phe Ala Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu	
160 165 170	
atc ttg atc ggc ctt ctt ttg att acg gat cgg tcg ctt cag gag acg	1061
Ile Leu Ile Gly Leu Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr	
175 180 185	

ctg atc aaa tgg atg acc ccg gtc gcc tcc ttc atg aaa aac cag tgg	1109
Leu Ile Lys Trp Met Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp	
190 195 200	
cag gcc ttt tta gca gat ctt aaa caa ttg aaa aac agc tcg ccg aaa	1157
Gln Ala Phe Leu Ala Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys	
205 210 215	
aag aaa tcc gga aaa aaa caa aag acg cag aga aaa ccg aaa gtg tct	1205
Lys Lys Ser Gly Lys Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser	
220 225 230 235	
gaa gag cct gta caa gaa gcg gac ctt gat cca gat ccg gtt att caa	1253
Glu Glu Pro Val Gln Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln	
240 245 250	
tca gaa ccg att att tca agc ttt tcc gac cgt gat gaa aag ccc gaa	1301
Ser Glu Pro Ile Ile Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu	
255 260 265	
gtt caa gct tac gaa gct ccg gcg gct cct gct gaa cct cct gct gag	1349
Val Gln Ala Tyr Glu Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu	
270 275 280	
ccc gaa atc ggt gag gaa atg cag gcc tcc ggc gcg ccc gaa atc acg	1397
Pro Glu Ile Gly Glu Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr	
285 290 295	
ttt aca gag cta gaa aac aag gat tac cag ctt ccg tcg att caa ttg	1445
Phe Thr Glu Leu Glu Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu	
300 305 310 315	
ctg gat gat ccg aag cac aca ggg cag cag gcg gat aaa aag aat att	1493
Leu Asp Asp Pro Lys His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile	
320 325 330	
tac gac aat gcc agg aag ctg gaa agg acg ttt caa agc ttc gga gtt	1541
Tyr Asp Asn Ala Arg Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val	
335 340 345	
aag gcg aaa gtc acc cag gtt cat ctc ggc ccg gcc gtc acg aaa tat	1589
Lys Ala Lys Val Thr Gln Val His Leu Gly Pro Ala Val Thr Lys Tyr	
350 355 360	
gaa gtc tat cct gat gtg ggc gtc aaa gtc agc aaa att gtc aac tta	1637
Glu Val Tyr Pro Asp Val Gly Val Lys Val Ser Lys Ile Val Asn Leu	
365 370 375	
agt gac gac ttg gct tta gcg ctc gcg gcc aag gat atc cgc atc gaa	1685
Ser Asp Asp Leu Ala Leu Ala Leu Ala Lys Asp Ile Arg Ile Glu	
380 385 390 395	
gcc ccg atc ccc gga aaa tcg gcg att gga atc gaa gtg ccg aat gcg	1733
Ala Pro Ile Pro Gly Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala	
400 405 410	



gaa gtg gcg atg gtt tcc ttg aaa gaa gtg ctt gaa tcg aaa ctg aat	1781
Glu Val Ala Met Val Ser Leu Lys Glu Val Leu Glu Ser Lys Leu Asn	
415 420 425	
gac cgg ccg gat gca aag ctg atg atc ggc ctc ggc cgg aac att tcc	1829
Asp Arg Pro Asp Ala Lys Leu Met Ile Gly Leu Gly Arg Asn Ile Ser	
430 435 440	
gga gaa gcg gta ttg gca gag ctg aac aaa atg ccc cac ctt ctt gtt	1877
Gly Glu Ala Val Leu Ala Glu Leu Asn Lys Met Pro His Leu Leu Val	
445 450 455	
gca gga gcg acc gga agc ggg aaa agc gtc tgt gtc aac ggg atc att	1925
Ala Gly Ala Thr Gly Ser Gly Lys Ser Val Cys Val Asn Gly Ile Ile	
460 465 470 475	
aca agc att ttg atg agg gca aag ccc cac gaa gtg aag atg atg atg	1973
Thr Ser Ile Leu Met Arg Ala Lys Pro His Glu Val Lys Met Met Met	
480 485 490	
att gat ccg aaa atg gtc gag ctc aat gtc tac aac ggg att ccg cat	2021
Ile Asp Pro Lys Met Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His	
495 500 505	
ttg ctc gct ccc gtc gtg aca gac ccg aaa aaa gca tcg cag gct ttg	2069
Leu Leu Ala Pro Val Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu	
510 515 520	
aag aaa gtc gtc aac gaa atg gag cgg cgc tac gaa ttg ttt tct cac	2117
Lys Lys Val Val Asn Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His	
525 530 535	
acg gga acg aga aat atc gaa ggg tat aac gac tat att aaa cgg atg	2165
Thr Gly Thr Arg Asn Ile Glu Gly Tyr Asn Asp Tyr Ile Lys Arg Met	
540 545 550 555	
aat gcc gca gaa gaa gca aag cag ccg gag ctt cca tac atc att gtg	2213
Asn Ala Ala Glu Glu Ala Lys Gln Pro Glu Leu Pro Tyr Ile Ile Val	
560 565 570	
att gtg gac gag ctt gcc gac ctg atg atg gtc gct tcc tct gat gtt	2261
Ile Val Asp Glu Leu Ala Asp Leu Met Met Val Ala Ser Ser Asp Val	
575 580 585	
gaa gac tcg atc aca agg ctt tcg caa atg gcc agg gcg gcg ggc atc	2309
Glu Asp Ser Ile Thr Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile	
590 595 600	
cac ctg atc att gcg acg cag agg cct tcg gtc gat gtt atc aca ggg	2357
His Leu Ile Ile Ala Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly	
605 610 615	
gtc att aaa gcc aac att ccg tca agg atc gct ttc agc gta tcg tct	2405
Val Ile Lys Ala Asn Ile Pro Ser Arg Ile Ala Phe Ser Val Ser Ser	
620 625 630 635	
cag acc gac tcc agg acg att ctt gat atg gga ggc gct gaa aaa ctt	2453

Gln Thr Asp Ser Arg Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu	
640 645 650	
ctc ggc aga ggg gac atg ctg ttt ctc cct gtc ggc gcc aat aaa ccg	2501
Leu Gly Arg Gly Asp Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro	
655 660 665	
ctc cgc gtt caa ggt gcc ttt ctg tca gac gaa gaa gtt gaa aaa gtt	2549
Leu Arg Val Gln Gly Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val	
670 675 680	
gtc gat cac gtc atc agc cag caa aaa gcc caa tac caa gaa gaa atg	2597
Val Asp His Val Ile Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met	
685 690 695	
att cca gaa gag acg cag gaa acg gtc agc gaa gtg aca gac gac ctt	2645
Ile Pro Glu Glu Thr Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu	
700 705 710 715	
tat gac gaa gcg gtc gca ctt gtg gtc agc atg cag acg gct tct gta	2693
Tyr Asp Glu Ala Val Ala Leu Val Val Ser Met Gln Thr Ala Ser Val	
720 725 730	
tcc atg ctg caa agg aga ttc cgc atc ggc tat aca aga gcg gcg cgg	2741
Ser Met Leu Gln Arg Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg	
735 740 745	
ctt atc gat gcc atg gaa gag cgg gga atc gtc ggc cca tat gaa gga	2789
Leu Ile Asp Ala Met Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly	
750 755 760	
tca aaa ccc cgt gaa gtt ctc ttg tca aaa gag caa tac gaa gaa ctc	2837
Ser Lys Pro Arg Glu Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu	
765 770 775	
tct tct tgagaagaga gttcttgttt aacataattt cattatgtaa actaaaaaac	2893
Ser Ser	
780	
atctatttat ttatttgaca aaacatgata tagttatcct caattaaaga taatttgaat	2953
ctgatctgtc agacggaggg aaaacatgtc gataaaaagct gacaatcaac ggttatgttt	3013
aaaggtgatt gatcggataa aagatgatat tcaaaaatggg gtcttttgcg aaaatgaacg	3073
gctcccgagt gaatttgagc tgtcaaagat gcttggtgtg agcagaacgg ctttgcgtga	3133
ggcgcttaga atactggaag aagaaaacgt catcatcaga aggcattggag tcggacattt	3193
tgtaaagtcc agaccgttat ttctatcagg tattgagcag ctgaacagcg tcacaaaaat	3253
gatcgagcag gcaagcatga cgccgggaac catttttatg tcctcacagg ttaccgctcc	3313
cactgaagaa gatatgctcc ggtttcaata tgc	3346

<210> 67

<211> 781  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 67

Met Ala Lys Arg Lys Arg Lys Ser Thr Lys Lys Gln Lys Gln Gly Lys  
 1 5 10 15

Lys Arg Ile His Leu Lys Phe Glu Leu Tyr Gly Leu Ile Cys Ile Ala  
 20 25 30

Ile Ser Ile Ile Ala Val Leu Gln Leu Gly Val Ala Gly Gln Thr Phe  
 35 40 45

Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp Phe Ile Leu Cys Leu  
 50 55 60

Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe Trp Lys Lys Lys Thr  
 65 70 75 80

Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu Tyr Cys Ile Ile Ala  
 85 90 95

Ser Met Leu Leu Leu Ser His Val Gln Leu Phe Gln His Leu Thr Glu  
 100 105 110

Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln Asn Thr Trp Glu Leu  
 115 120 125

Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser Pro Asp Leu Gly Gly  
 130 135 140

Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser Tyr Phe Leu Phe Ala  
 145 150 155 160

Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu Ile Leu Ile Gly Leu  
 165 170 175

Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr Leu Ile Lys Trp Met  
 180 185 190

Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp Gln Ala Phe Leu Ala  
 195 200 205

Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys Lys Lys Ser Gly Lys  
 210 215 220

Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser Glu Glu Pro Val Gln  
 225 230 235 240

Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln Ser Glu Pro Ile Ile  
 245 250 255

Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu Val Gln Ala Tyr Glu  
 260 265 270

Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu Pro Glu Ile Gly Glu  
 275 280 285

Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr Phe Thr Glu Leu Glu  
 290 295 300

Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu Leu Asp Asp Pro Lys  
 305 310 315 320

His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile Tyr Asp Asn Ala Arg  
 325 330 335

Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val Lys Ala Lys Val Thr  
 340 345 350

Gln Val His Leu Gly Pro Ala Val Thr Lys Tyr Glu Val Tyr Pro Asp  
 355 360 365

Val Gly Val Lys Val Ser Lys Ile Val Asn Leu Ser Asp Asp Leu Ala  
 370 375 380

Leu Ala Leu Ala Ala Lys Asp Ile Arg Ile Glu Ala Pro Ile Pro Gly  
 385 390 395 400

Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala Glu Val Ala Met Val  
 405 410 415

Ser Leu Lys Glu Val Leu Glu Ser Lys Leu Asn Asp Arg Pro Asp Ala  
 420 425 430

Lys Leu Met Ile Gly Leu Gly Arg Asn Ile Ser Gly Glu Ala Val Leu  
435 440 445

Ala Glu Leu Asn Lys Met Pro His Leu Leu Val Ala Gly Ala Thr Gly  
450 455 460

Ser Gly Lys Ser Val Cys Val Asn Gly Ile Ile Thr Ser Ile Leu Met  
465 470 475 480

Arg Ala Lys Pro His Glu Val Lys Met Met Met Ile Asp Pro Lys Met  
485 490 495

Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His Leu Leu Ala Pro Val  
500 505 510

Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu Lys Lys Val Val Asn  
515 520 525

Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His Thr Gly Thr Arg Asn  
530 535 540

Ile Glu Gly Tyr Asn Asp Tyr Ile Lys Arg Met Asn Ala Ala Glu Glu  
545 550 555 560

Ala Lys Gln Pro Glu Leu Pro Tyr Ile Ile Val Ile Val Asp Glu Leu  
565 570 575

Ala Asp Leu Met Met Val Ala Ser Ser Asp Val Glu Asp Ser Ile Thr  
580 585 590

Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile His Leu Ile Ile Ala  
595 600 605

Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly Val Ile Lys Ala Asn  
610 615 620

Ile Pro Ser Arg Ile Ala Phe Ser Val Ser Ser Gln Thr Asp Ser Arg  
625 630 635 640

Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu Leu Gly Arg Gly Asp  
645 650 655

Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro Leu Arg Val Gln Gly

660	665	670
Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val Val Asp His Val Ile		
675	680	685
Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met Ile Pro Glu Glu Thr		
690	695	700
Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu Tyr Asp Glu Ala Val		
705	710	715
Ala Leu Val Val Ser Met Gln Thr Ala Ser Val Ser Met Leu Gln Arg		
725	730	735
Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg Leu Ile Asp Ala Met		
740	745	750
Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly Ser Lys Pro Arg Glu		
755	760	765
Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu Ser Ser		
770	775	780

<210> 68  
 <211> 1045  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1043)

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atcaatgaac ctgtcatttt cggacttccg gtcgtgctca atccaatctt catgattccc	120
tttattatcg ttccggcagt caatactgtc atcggctatt tgttcatcaa gtttcagctg	180
attccgccga tcgcatacgc tgttccgtgg acaacgccag ggccggtgat tccgtttctc	240
gggaccggag gaaactggct tgcgctcggc gtcggctttc tctgcctcgc catttcaacg	300
atgatttatc tgccgtttgt gatggctgcc aacaagactg tgaatacggg cagggagcat	360
tccgcggaaa acaggaagga atcataactt tagacggggc gcctttttacg ggcgcccgtc	420
tttttttaaa aaaagtcatg cggctctctt ttctctcata caatctatta aaatcaaaag	480

cacgtctggg aggaagatac atg cgg aag ccc aca atc aaa gag ctc atc ttt	533
Met Arg Lys Pro Thr Ile Lys Glu Leu Ile Phe	
1 5 10	
caa cat atg aag gac cat ctg tcg atc tat tta ttt gtt tct gtg ctg	581
Gln His Met Lys Asp His Leu Ser Ile Tyr Leu Phe Val Ser Val Leu	
15 20 25	
ttc tta atg ggt gtg att ttc ggc gcg gtc atc gtc aac agc atg acg	629
Phe Leu Met Gly Val Ile Phe Gly Ala Val Ile Val Asn Ser Met Thr	
30 35 40	
atc ggt caa aaa gaa gat ttg ttc tac tat ttg aat caa ttt ttt gga	677
Ile Gly Gln Lys Glu Asp Leu Phe Tyr Tyr Leu Asn Gln Phe Phe Gly	
45 50 55	
cag ctt tcc gaa gga aaa gca gcc agc tca aag gaa atg ttt ttg cag	725
Gln Leu Ser Glu Gly Lys Ala Ala Ser Ser Lys Glu Met Phe Leu Gln	
60 65 70 75	
agc ttt ctt cat aat atg aaa tat tta ggc tta atg tgg att ctc ggg	773
Ser Phe Leu His Asn Met Lys Tyr Leu Gly Leu Met Trp Ile Leu Gly	
80 85 90	
ata tcc atc atc ggt ctg ccc gtc att ttt atc atg gtc ttc tta aaa	821
Ile Ser Ile Ile Gly Leu Pro Val Ile Phe Ile Met Val Phe Leu Lys	
95 100 105	
ggg atc gtc gtc gga ttt aca gtc ggc ttt ttg gtc aat caa atg gga	869
Gly Ile Val Val Gly Phe Thr Val Gly Phe Leu Val Asn Gln Met Gly	
110 115 120	
atc aac ggc ttt ttc ctg tct ttt gtc tcc gtg ctc ccg caa aat att	917
Ile Asn Gly Phe Phe Leu Ser Phe Val Ser Val Leu Pro Gln Asn Ile	
125 130 135	
ctg ctg atc ccg gcg tac ttg atc atg ggc acc tgc gcc atc gcc ttt	965
Leu Leu Ile Pro Ala Tyr Leu Ile Met Gly Thr Cys Ala Ile Ala Phe	
140 145 150 155	
tcg atg agg ctc atc cgc cag ctt ttt gta aac gca gcc ttc aga agc	1013
Ser Met Arg Leu Ile Arg Gln Leu Phe Val Asn Ala Ala Phe Arg Ser	
160 165 170	
acc tgt cca tgt gtt gtg ccg cgg gta gcc ga	1045
Thr Cys Pro Cys Val Val Pro Arg Val Ala	
175 180	

<210> 69  
 <211> 181  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 69

Met Arg Lys Pro Thr Ile Lys Glu Leu Ile Phe Gln His Met Lys Asp  
 1 5 10 15

His Leu Ser Ile Tyr Leu Phe Val Ser Val Leu Phe Leu Met Gly Val  
 20 25 30

Ile Phe Gly Ala Val Ile Val Asn Ser Met Thr Ile Gly Gln Lys Glu  
 35 40 45

Asp Leu Phe Tyr Tyr Leu Asn Gln Phe Phe Gly Gln Leu Ser Glu Gly  
 50 55 60

Lys Ala Ala Ser Ser Lys Glu Met Phe Leu Gln Ser Phe Leu His Asn  
 65 70 75 80

Met Lys Tyr Leu Gly Leu Met Trp Ile Leu Gly Ile Ser Ile Ile Gly  
 85 90 95

Leu Pro Val Ile Phe Ile Met Val Phe Leu Lys Gly Ile Val Val Gly  
 100 105 110

Phe Thr Val Gly Phe Leu Val Asn Gln Met Gly Ile Asn Gly Phe Phe  
 115 120 125

Leu Ser Phe Val Ser Val Leu Pro Gln Asn Ile Leu Leu Ile Pro Ala  
 130 135 140

Tyr Leu Ile Met Gly Thr Cys Ala Ile Ala Phe Ser Met Arg Leu Ile  
 145 150 155 160

Arg Gln Leu Phe Val Asn Ala Ala Phe Arg Ser Thr Cys Pro Cys Val  
 165 170 175

Val Pro Arg Val Ala  
 180

<210> 70  
 <211> 1108  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (500)..(1108)



[illegible]

aga gct tca agg gaa aca gaa aaa gaa aac aga cgg gga aaa acc tcc	1012
Arg Ala Ser Arg Glu Thr Glu Lys Glu Asn Arg Arg Gly Lys Thr Ser	
160 165 170	

tca aca atc gac ggg cgg ccg caa agt cgt att tat cta caa tac gca	1060
Ser Thr Ile Asp Gly Arg Pro Gln Ser Arg Ile Tyr Leu Gln Tyr Ala	
175 180 185	

caa tac gga atc gta tct tcc cct ttt aaa agg tca ggc aga tcc ttt	1108
Gln Tyr Gly Ile Val Ser Ser Pro Phe Lys Arg Ser Gly Arg Ser Phe	
190 195 200	

<210> 71  
 <211> 203  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 71

Asn Glu Lys Lys Arg Gln Glu Ser Ser Val Cys Ala Gly Cys Lys Trp
1 5 10 15

Lys Lys Arg Gly Ser Asp Ser Ile Leu Ile Tyr Arg Gln Pro Ala Ala
20 25 30

Arg Phe Tyr Phe Ile Arg Arg Ala His Ile Ala Ala Ser Ser Val Lys
35 40 45

Ala Val Phe Ile Val Val Pro Gly Gly Ser Ser Thr Glu Gly Arg Asp
50 55 60

Leu Trp Ala His Phe Gly Asn Gly Lys Pro Leu Leu Cys Ile Arg Ile
65 70 75 80

Ala Gly Thr Glu Ser Ala Leu Ser Ala Phe Pro Pro Arg Pro Glu Ala
85 90 95

Gly Asp Gln His Ser Phe Glu Arg Ser Ala Lys Phe Ser Arg Thr Gly
100 105 110

Ala Ser Gly Ile Leu Ser Phe Ser Leu Gly Asn Pro His Cys Arg Ala
115 120 125

Arg Asp Gly Leu Tyr Glu Tyr Ala Val Arg Ile Ser Ala Ala Asp Ser
130 135 140

Gly Leu Lys Arg Gly Glu Arg Ser Glu Ser Cys Arg Ala Ser Arg Glu  
 145 150 155 160

Thr Glu Lys Glu Asn Arg Arg Gly Lys Thr Ser Ser Thr Ile Asp Gly  
 165 170 175

Arg Pro Gln Ser Arg Ile Tyr Leu Gln Tyr Ala Gln Tyr Gly Ile Val  
 180 185 190

Ser Ser Pro Phe Lys Arg Ser Gly Arg Ser Phe  
 195 200

<210> 72  
 <211> 1152  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (107)..(985)

<400> 72  
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taaaagtata aatttcatga agagggttca gaatggtgct gaggtg atg agt aag 115  
 Met Ser Lys  
 1

aaa gag aaa gag aag aat cgt act tcc aaa atc aca aag ttg caa caa 163  
 Lys Glu Lys Glu Lys Asn Arg Thr Ser Lys Ile Thr Lys Leu Gln Gln  
 5 10 15

ttt ttt cgt aaa cgc tgg gta ttt ccg gcc atc tat ttg aca agt gcc 211  
 Phe Phe Arg Lys Arg Trp Val Phe Pro Ala Ile Tyr Leu Thr Ser Ala  
 20 25 30 35

gtc gtt gta tta acc gcc gtt cta tgg tat caa tcg gct tct aac aac 259  
 Val Val Val Leu Thr Ala Val Leu Trp Tyr Gln Ser Ala Ser Asn Asn  
 40 45 50

gat gta aaa gac cag ctt gca gac gat ggc aag aaa tca gcc tat gat 307  
 Asp Val Lys Asp Gln Leu Ala Asp Asp Gly Lys Lys Ser Ala Tyr Asp  
 55 60 65

aac cgg gat gat gcg gta gaa gta ggc aaa cca gtc gaa aat gtc gca 355  
 Asn Arg Asp Asp Ala Val Glu Val Gly Lys Pro Val Glu Asn Val Ala  
 70 75 80

atg ccg gtt gct gat tct gaa aat gtt tcc gtc gtt aaa aag ttt ttt 403  
 Met Pro Val Ala Asp Ser Glu Asn Val Ser Val Val Lys Lys Phe Phe  
 85 90 95

gaa act gac gca act aaa gaa gag aaa gaa gca gca ctt gta aac tat	451
Glu Thr Asp Ala Thr Lys Glu Glu Lys Glu Ala Ala Leu Val Asn Tyr	
100 105 110 115	
aat aac acg tac agc atg agc aaa ggt atc gac ttg gct gag aaa gac	499
Asn Asn Thr Tyr Ser Met Ser Lys Gly Ile Asp Leu Ala Glu Lys Asp	
120 125 130	
gga aaa aca ttt gat gtt tcc gca tct cta agc ggt acg gtc atc aaa	547
Gly Lys Thr Phe Asp Val Ser Ala Ser Leu Ser Gly Thr Val Ile Lys	
135 140 145	
gct gca aaa gac cct gta ctg ggc tac gtt gtt gaa gtt gaa cat gaa	595
Ala Ala Lys Asp Pro Val Leu Gly Tyr Val Val Glu Val Glu His Glu	
150 155 160	
gat ggt tta tca act gtg tat cag tct ctt tct gaa gta agc gtc aaa	643
Asp Gly Leu Ser Thr Val Tyr Gln Ser Leu Ser Glu Val Ser Val Lys	
165 170 175	
caa ggt gac aag att gaa caa aat caa gtc atc gga aaa gca ggc aaa	691
Gln Gly Asp Lys Ile Glu Gln Asn Gln Val Ile Gly Lys Ala Gly Lys	
180 185 190 195	
aac ctt tac aat gaa gaa ggc gga aac cat gtg cat ttt gaa atc cgc	739
Asn Leu Tyr Asn Glu Glu Gly Gly Asn His Val His Phe Glu Ile Arg	
200 205 210	
aaa gac ggt gtt gcg cta aac ccg ctg aac ttc atg gac aag ccg gtc	787
Lys Asp Gly Val Ala Leu Asn Pro Leu Asn Phe Met Asp Lys Pro Val	
215 220 225	
tcc agc att gaa aaa gca atg gag gaa caa gcg tct gaa gtg aaa gaa	835
Ser Ser Ile Glu Lys Ala Met Glu Glu Gln Ala Ser Glu Val Lys Glu	
230 235 240	
cct gct cag cct tct gtt gaa gaa aag tca aaa aca gaa gac aaa gcg	883
Pro Ala Gln Pro Ser Val Glu Glu Lys Ser Lys Thr Glu Asp Lys Ala	
245 250 255	
aaa gat caa aca gat gga aaa gac gac aaa acc aag cgg gaa gat tcg	931
Lys Asp Gln Thr Asp Gly Lys Asp Asp Lys Thr Lys Arg Glu Asp Ser	
260 265 270 275	
tct gaa ggg tca gaa aat caa gac gga acc cag tct gac gat tca agc	979
Ser Glu Gly Ser Glu Asn Gln Asp Gly Thr Gln Ser Asp Asp Ser Ser	
280 285 290	
cag tca taaggcacgc ttccctcagg gcgcctatca aatgcgatag gcgccttttt	1035
Gln Ser	
tggtacaatc aaaaaaaacc cgtatcaaat cggcggagcc agccgtttttt aagtaagagg	1095
cctctttaag gagtggaagg cattaggaag taagtagaac agcaaaccgc ctagtaa	1152

<210> 73  
 <211> 293  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 73

Met Ser Lys Lys Glu Lys Glu Lys Asn Arg Thr Ser Lys Ile Thr Lys  
 1 5 10 15

Leu Gln Gln Phe Phe Arg Lys Arg Trp Val Phe Pro Ala Ile Tyr Leu  
 20 25 30

Thr Ser Ala Val Val Val Leu Thr Ala Val Leu Trp Tyr Gln Ser Ala  
 35 40 45

Ser Asn Asn Asp Val Lys Asp Gln Leu Ala Asp Asp Gly Lys Lys Ser  
 50 55 60

Ala Tyr Asp Asn Arg Asp Asp Ala Val Glu Val Gly Lys Pro Val Glu  
 65 70 75 80

Asn Val Ala Met Pro Val Ala Asp Ser Glu Asn Val Ser Val Val Lys  
 85 90 95

Lys Phe Phe Glu Thr Asp Ala Thr Lys Glu Glu Lys Glu Ala Ala Leu  
 100 105 110

Val Asn Tyr Asn Asn Thr Tyr Ser Met Ser Lys Gly Ile Asp Leu Ala  
 115 120 125

Glu Lys Asp Gly Lys Thr Phe Asp Val Ser Ala Ser Leu Ser Gly Thr  
 130 135 140

Val Ile Lys Ala Ala Lys Asp Pro Val Leu Gly Tyr Val Val Glu Val  
 145 150 155 160

Glu His Glu Asp Gly Leu Ser Thr Val Tyr Gln Ser Leu Ser Glu Val  
 165 170 175

Ser Val Lys Gln Gly Asp Lys Ile Glu Gln Asn Gln Val Ile Gly Lys  
 180 185 190

Ala Gly Lys Asn Leu Tyr Asn Glu Glu Gly Gly Asn His Val His Phe  
 195 200 205

Glu Ile Arg Lys Asp Gly Val Ala Leu Asn Pro Leu Asn Phe Met Asp  
 210 215 220

Lys Pro Val Ser Ser Ile Glu Lys Ala Met Glu Glu Gln Ala Ser Glu  
 225 230 235 240

Val Lys Glu Pro Ala Gln Pro Ser Val Glu Glu Lys Ser Lys Thr Glu  
 245 250 255

Asp Lys Ala Lys Asp Gln Thr Asp Gly Lys Asp Asp Lys Thr Lys Arg  
 260 265 270

Glu Asp Ser Ser Glu Gly Ser Glu Asn Gln Asp Gly Thr Gln Ser Asp  
 275 280 285

Asp Ser Ser Gln Ser  
 290

<210> 74  
 <211> 1747  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1244)

<400> 74  
 gctttaatcg cgggtaactt gcacagtaca accgacatcc cgttctgggt gcagtttgca 60  
 tgcgccatgg ccatgggact cggaacatct gtcggcggct ggaaaatcat caaaaccgtc 120  
 ggcggaaaaa tcatgaagat ccgtcccgtc aacggtgtct ctgcagattt gacgggagcc 180  
 ctcatcatct ttggcgcgac gatcgtccat ttgcctgtca gcacgacaca cgtcattttct 240  
 tcatccattt taggcgtggg cgcttcccac cgggtgaaag gcgtaaaactg gggcaccgca 300  
 aagcggatgc tgatcacttg ggtcattacc cttcccattt cggcaaccat cgggtgcattt 360  
 gcctatttca tacttgattt attcttttaa tcagcacact cccgtccgaa tctaggacgg 420  
 gagttttcat gtttaaaaga aagccggcat aacaatagaa ataggaactg cactattttct 480  
 cggggaagagg gaaacaagtt atg ctg cta ttt tat caa ttc ctt gtt tgg ctt 533  
 Met Leu Leu Phe Tyr Gln Phe Leu Val Trp Leu  
 1 5 10

att gtt ttg gcg ctg gct ctg tac gta gct gcc gtg tgg cgt ttt gaa Ile Val Leu Ala Leu Ala Leu Tyr Val Ala Ala Val Trp Arg Phe Glu 15 20 25	581
aaa cag ctc gcc gaa aaa acg gtc gcc atc aga aaa acg tgg tac ctt Lys Gln Leu Ala Glu Lys Thr Val Ala Ile Arg Lys Thr Trp Tyr Leu 30 35 40	629
ctt tat gtc atc ggc gcc gtg ata tat tgg acg cac gat ccg cag tca Leu Tyr Val Ile Gly Ala Val Ile Tyr Trp Thr His Asp Pro Gln Ser 45 50 55	677
att ttc aca aac ccg ctt cat tac ctg atc gtt gcc gtt ttt ttc acg Ile Phe Thr Asn Pro Leu His Tyr Leu Ile Val Ala Val Phe Phe Thr 60 65 70 75	725
ttg aca gac gct ttt att ttc tta aat gcc tac ttt aaa aag ctc ggc Leu Thr Asp Ala Phe Ile Phe Leu Asn Ala Tyr Phe Lys Lys Leu Gly 80 85 90	773
agc tct gaa ctc gcg aca gat aca aga atg ctt ctc gaa gaa aac aac Ser Ser Glu Leu Ala Thr Asp Thr Arg Met Leu Leu Glu Glu Asn Asn 95 100 105	821
gac ctc ctc cac acg tat caa aac agg ctg aaa acg ttt caa tac cta Asp Leu Leu His Thr Tyr Gln Asn Arg Leu Lys Thr Phe Gln Tyr Leu 110 115 120	869
ttg aaa aac gaa ccg atc cac atc tat tat gga aat ata gaa gcg tat Leu Lys Asn Glu Pro Ile His Ile Tyr Tyr Gly Asn Ile Glu Ala Tyr 125 130 135	917
gca gaa ggc atc gaa aag ctc atc aaa cgg ttt gcc gaa aaa atg aat Ala Glu Gly Ile Glu Lys Leu Ile Lys Arg Phe Ala Glu Lys Met Asn 140 145 150 155	965
ata tcc gct gca ctt tgc gaa tat aat tca gaa gaa agc aag gat cat Ile Ser Ala Ala Leu Cys Glu Tyr Asn Ser Glu Glu Ser Lys Asp His 160 165 170	1013
ttg ctt gag cat atg gaa aac cgg ttc gat gtt caa gaa aag ctt gac Leu Leu Glu His Met Glu Asn Arg Phe Asp Val Gln Glu Lys Leu Asp 175 180 185	1061
cgc aaa gac gtt tat tat gaa gaa aac gga aaa atg gtc ctc att cct Arg Lys Asp Val Tyr Tyr Glu Glu Asn Gly Lys Met Val Leu Ile Pro 190 195 200	1109
ttt tcc atc cac gat ttt gac tat gtc atg aag tta acc tca gaa gac Phe Ser Ile His Asp Phe Asp Tyr Val Met Lys Leu Thr Ser Glu Asp 205 210 215	1157
ctt gtc aca gaa ttt gat tat ctc ctg ttt act tct tta aca agc atc Leu Val Thr Glu Phe Asp Tyr Leu Leu Phe Thr Ser Leu Thr Ser Ile 220 225 230 235	1205
tat gat ctt ctg cta cca aac gaa gag gaa ggt gac gac tgatggagcc	1254

Tyr Asp Leu Leu Leu Pro Asn Glu Glu Glu Gly Asp Asp  
 240 245  
 tgcttttcag caagaccagg aaagcgtaaa aaagcgcctc gccttttaaaa tgttttaaag 1314  
 gcaatccaaa accaatatcg cgaaatacga agtcagcccc tataccgaac ggattttccg 1374  
 gcaaaacgaa cggctgatcg gcgagtataa aagaaaaaaa gcttaacgag gacgggaaaa 1434  
 aaattctccc gtccttattc cgtttttcccg tttcttacat acaataaacc aatcaactaa 1494  
 accgctgaat taggtgatgc tgtgaaaaaa ctgaaaaaac aagtcaaaca cgtcgatttc 1554  
 gcaaaattcg gcctgtcaga ctatacctct cttctcagaa gaagaagcga aaaaatcatt 1614  
 aaaacgctga acagaagaaa aaacaaaaccg tgaagcttgg actttcaccc tccttctctg 1674  
 ctgagaaggg gggttatatt catgtctaca ggagcatcat aaaggatgcc cctgtccgcc 1734  
 ttctcctaca gat 1747

<210> 75  
 <211> 248  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 75

Met Leu Leu Phe Tyr Gln Phe Leu Val Trp Leu Ile Val Leu Ala Leu  
 1 5 10 15

Ala Leu Tyr Val Ala Ala Val Trp Arg Phe Glu Lys Gln Leu Ala Glu  
 20 25 30

Lys Thr Val Ala Ile Arg Lys Thr Trp Tyr Leu Leu Tyr Val Ile Gly  
 35 40 45

Ala Val Ile Tyr Trp Thr His Asp Pro Gln Ser Ile Phe Thr Asn Pro  
 50 55 60

Leu His Tyr Leu Ile Val Ala Val Phe Phe Thr Leu Thr Asp Ala Phe  
 65 70 75 80

Ile Phe Leu Asn Ala Tyr Phe Lys Lys Leu Gly Ser Ser Glu Leu Ala  
 85 90 95

Thr Asp Thr Arg Met Leu Leu Glu Glu Asn Asn Asp Leu Leu His Thr  
 100 105 110



Tyr Gln Asn Arg Leu Lys Thr Phe Gln Tyr Leu Leu Lys Asn Glu Pro  
115 120 125

Ile His Ile Tyr Tyr Gly Asn Ile Glu Ala Tyr Ala Glu Gly Ile Glu  
130 135 140

Lys Leu Ile Lys Arg Phe Ala Glu Lys Met Asn Ile Ser Ala Ala Leu  
145 150 155 160

Cys Glu Tyr Asn Ser Glu Glu Ser Lys Asp His Leu Leu Glu His Met  
165 170 175

Glu Asn Arg Phe Asp Val Gln Glu Lys Leu Asp Arg Lys Asp Val Tyr  
180 185 190

Tyr Glu Glu Asn Gly Lys Met Val Leu Ile Pro Phe Ser Ile His Asp  
195 200 205

Phe Asp Tyr Val Met Lys Leu Thr Ser Glu Asp Leu Val Thr Glu Phe  
210 215 220

Asp Tyr Leu Leu Phe Thr Ser Leu Thr Ser Ile Tyr Asp Leu Leu Leu  
225 230 235 240

Pro Asn Glu Glu Glu Gly Asp Asp  
245

<210> 76  
<211> 2020  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(1742)

<400> 76  
gattcactca tacgccatga gtgaaattga gccattggaa acaactatca agacgtatga 60  
agttgagtta gaggaattaa aaacgaagag aaaagaactt ataaattgga ggctaaaaga 120  
tattatttca gaagagattt taaaagagga aatggaagat ttacgagagg aagaaaaatt 180  
aataataact cgaattgaaa aattacagca cctcattaaa ctcagagata aaaccttttt 240  
aaccaatatc atttcaactt cactacagca tctaaagaac tttttcaata ttatcgaaga 300

tgatgacaaa aaggaattac ttcgttctct cattgaagag attcacgtaa atccaggaaa	360
aactactaag gatagaacga tcaaagaagt gatttataag tttgatttaa aatatttgaa	420
atcaattgaa ctaagagaag gggaacatct tttctctttt ttgtgtttca tattataatt	480
acaaggaagg gaggattatt atg cac gaa ata aaa cgt gtc gca att tac tgt	533
Met His Glu Ile Lys Arg Val Ala Ile Tyr Cys	
1 5 10	
aga gtt tct acc gaa gag cag gca acg gaa gga tac agc ata tct gcc	581
Arg Val Ser Thr Glu Glu Gln Ala Thr Glu Gly Tyr Ser Ile Ser Ala	
15 20 25	
caa tta caa act tta cgt caa tat act cag tta tat ggt tgg gag att	629
Gln Leu Gln Thr Leu Arg Gln Tyr Thr Gln Leu Tyr Gly Trp Glu Ile	
30 35 40	
gca gag gaa tat gta gat gag gga ata agt gga aag aac att agc ggt	677
Ala Glu Glu Tyr Val Asp Glu Gly Ile Ser Gly Lys Asn Ile Ser Gly	
45 50 55	
cgc cct gca atg caa aaa ctt att tca gat gtt gaa aag gat aaa ttt	725
Arg Pro Ala Met Gln Lys Leu Ile Ser Asp Val Glu Lys Asp Lys Phe	
60 65 70 75	
caa gct gtt ctt gtt tgg aag atc tca cgc cta tca cga aat atg tta	773
Gln Ala Val Leu Val Trp Lys Ile Ser Arg Leu Ser Arg Asn Met Leu	
80 85 90	
gat act ctc act cta tta gac aaa ttc gaa gat tat gga gta aag ttc	821
Asp Thr Leu Thr Leu Leu Asp Lys Phe Glu Asp Tyr Gly Val Lys Phe	
95 100 105	
atc tct tac tct gaa aac ttt gat aca ggc agt cca att ggt cgt tta	869
Ile Ser Tyr Ser Glu Asn Phe Asp Thr Gly Ser Pro Ile Gly Arg Leu	
110 115 120	
gtt gtt caa cta atg gct tcc att gca gaa atg gag cgt aat acg tta	917
Val Val Gln Leu Met Ala Ser Ile Ala Glu Met Glu Arg Asn Thr Leu	
125 130 135	
tct gag aac gtt aag ctc gga atg aaa cag aga gca tta gaa ggt tca	965
Ser Glu Asn Val Lys Leu Gly Met Lys Gln Arg Ala Leu Glu Gly Ser	
140 145 150 155	
tgg aat gga ggc gtt gta ttt ggc tac gat aca att gaa aaa gag ctt	1013
Trp Asn Gly Gly Val Val Phe Gly Tyr Asp Thr Ile Glu Lys Glu Leu	
160 165 170	
gtg atc aac aaa aag gaa gct gag att gta caa caa atc tat caa cta	1061
Val Ile Asn Lys Lys Glu Ala Glu Ile Val Gln Gln Ile Tyr Gln Leu	
175 180 185	
tat gcc aat ggt aaa ggc tta aag tca atc gca aac tac tta aat aaa	1109
Tyr Ala Asn Gly Lys Gly Leu Lys Ser Ile Ala Asn Tyr Leu Asn Lys	
190 195 200	

gca ggt tac aga act aaa cgg aat tgt tat ttt tcg ata aac ggt gta	1157
Ala Gly Tyr Arg Thr Lys Arg Asn Cys Tyr Phe Ser Ile Asn Gly Val	
205 210 215	
gct caa atc tta gac aat gtt atc tat aac ggg aag atc agt tgg tta	1205
Ala Gln Ile Leu Asp Asn Val Ile Tyr Asn Gly Lys Ile Ser Trp Leu	
220 225 230 235	
aaa gtt gaa aat tgg gat aca aaa cgg agg aga ggg aaa aat cca aat	1253
Lys Val Glu Asn Trp Asp Thr Lys Arg Arg Arg Gly Lys Asn Pro Asn	
240 245 250	
cct atc ctt gta gaa gga cag cat gaa gcc att att tcc gat gaa tta	1301
Pro Ile Leu Val Glu Gly Gln His Glu Ala Ile Ile Ser Asp Glu Leu	
255 260 265	
tgg agt atg gta caa gca agg cgg aaa agt aaa tca ttt aaa caa agg	1349
Trp Ser Met Val Gln Ala Arg Arg Lys Ser Lys Ser Phe Lys Gln Arg	
270 275 280	
caa tct aat gaa cca ttt tta ctt agc agt ctt tta cgt tgc ccc gat	1397
Gln Ser Asn Glu Pro Phe Leu Leu Ser Ser Leu Leu Arg Cys Pro Asp	
285 290 295	
tgt ggt caa ggt atg gtt cct gcc att aca aca aat aaa cga aag gat	1445
Cys Gly Gln Gly Met Val Pro Ala Ile Thr Thr Asn Lys Arg Lys Asp	
300 305 310 315	
gga aca aag aag aaa tat cgt tat tat gtt tgc tct aac ttt cat aac	1493
Gly Thr Lys Lys Lys Tyr Arg Tyr Tyr Val Cys Ser Asn Phe His Asn	
320 325 330	
aaa ggt tca tct gca tgt aga gca aat tca ata aaa gca tat gat gca	1541
Lys Gly Ser Ser Ala Cys Arg Ala Asn Ser Ile Lys Ala Tyr Asp Ala	
335 340 345	
gaa tac gaa gta att aat aag att gag aag atc ctt tcc aac caa aat	1589
Glu Tyr Glu Val Ile Asn Lys Ile Glu Lys Ile Leu Ser Asn Gln Asn	
350 355 360	
cag tta ttc tct aaa ctt caa tct ata aat act act tcg att gaa tct	1637
Gln Leu Phe Ser Lys Leu Gln Ser Ile Asn Thr Thr Ser Ile Glu Ser	
365 370 375	
tta aac caa ctc aat agt gaa ttg aaa caa tta gaa aat cgc cta tca	1685
Leu Asn Gln Leu Asn Ser Glu Leu Lys Gln Leu Glu Asn Arg Leu Ser	
380 385 390 395	
gaa ata caa gag tac aga atc gtt act tgg aag cat ttg agc aaa aga	1733
Glu Ile Gln Glu Tyr Arg Ile Val Thr Trp Lys His Leu Ser Lys Arg	
400 405 410	
cct tac caa tagcaatctt gcaagaacga ttacagcatg tctctaaaga	1782
Pro Tyr Gln	

aaaagcagag ttagaacaaa ggcacaatga atcactgggc aattaagctc gaacgatgca 1842  
 aaagtaataa aaccagaact gattcaaaag ctttagaaaa aattccttta gtctataaac 1902  
 atcatcaaga gaaagcaaaa cagttactca acttttgctt ataaattaca gtaagcatca 1962  
 atgggtcatc acgattgtcg atcaattgaa ctcgactttg actttcagaa gtcattatt 2020

<210> 77  
 <211> 414  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 77

Met His Glu Ile Lys Arg Val Ala Ile Tyr Cys Arg Val Ser Thr Glu  
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Glu Gln Ala Thr Glu Gly Tyr Ser Ile Ser Ala Gln Leu Gln Thr Leu  
 20 25 30

Arg Gln Tyr Thr Gln Leu Tyr Gly Trp Glu Ile Ala Glu Glu Tyr Val  
 35 40 45

Asp Glu Gly Ile Ser Gly Lys Asn Ile Ser Gly Arg Pro Ala Met Gln  
 50 55 60

Lys Leu Ile Ser Asp Val Glu Lys Asp Lys Phe Gln Ala Val Leu Val  
 65 70 75 80

Trp Lys Ile Ser Arg Leu Ser Arg Asn Met Leu Asp Thr Leu Thr Leu  
 85 90 95

Leu Asp Lys Phe Glu Asp Tyr Gly Val Lys Phe Ile Ser Tyr Ser Glu  
 100 105 110

Asn Phe Asp Thr Gly Ser Pro Ile Gly Arg Leu Val Val Gln Leu Met  
 115 120 125

Ala Ser Ile Ala Glu Met Glu Arg Asn Thr Leu Ser Glu Asn Val Lys  
 130 135 140

Leu Gly Met Lys Gln Arg Ala Leu Glu Gly Ser Trp Asn Gly Gly Val  
 145 150 155 160

Val Phe Gly Tyr Asp Thr Ile Glu Lys Glu Leu Val Ile Asn Lys Lys

165	170	175
Glu Ala Glu Ile Val Gln Gln Ile Tyr Gln Leu Tyr Ala Asn Gly Lys 180 185 190		
Gly Leu Lys Ser Ile Ala Asn Tyr Leu Asn Lys Ala Gly Tyr Arg Thr 195 200 205		
Lys Arg Asn Cys Tyr Phe Ser Ile Asn Gly Val Ala Gln Ile Leu Asp 210 215 220		
Asn Val Ile Tyr Asn Gly Lys Ile Ser Trp Leu Lys Val Glu Asn Trp 225 230 235 240		
Asp Thr Lys Arg Arg Arg Gly Lys Asn Pro Asn Pro Ile Leu Val Glu 245 250 255		
Gly Gln His Glu Ala Ile Ile Ser Asp Glu Leu Trp Ser Met Val Gln 260 265 270		
Ala Arg Arg Lys Ser Lys Ser Phe Lys Gln Arg Gln Ser Asn Glu Pro 275 280 285		
Phe Leu Leu Ser Ser Leu Leu Arg Cys Pro Asp Cys Gly Gln Gly Met 290 295 300		
Val Pro Ala Ile Thr Thr Asn Lys Arg Lys Asp Gly Thr Lys Lys Lys 305 310 315 320		
Tyr Arg Tyr Tyr Val Cys Ser Asn Phe His Asn Lys Gly Ser Ser Ala 325 330 335		
Cys Arg Ala Asn Ser Ile Lys Ala Tyr Asp Ala Glu Tyr Glu Val Ile 340 345 350		
Asn Lys Ile Glu Lys Ile Leu Ser Asn Gln Asn Gln Leu Phe Ser Lys 355 360 365		
Leu Gln Ser Ile Asn Thr Thr Ser Ile Glu Ser Leu Asn Gln Leu Asn 370 375 380		
Ser Glu Leu Lys Gln Leu Glu Asn Arg Leu Ser Glu Ile Gln Glu Tyr 385 390 395 400		

Arg Ile Val Thr Trp Lys His Leu Ser Lys Arg Pro Tyr Gln  
 405 410

<210> 78  
 <211> 1417  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (510)..(1298)

<400> 78  
 tgcggaacatc cgcttgcttt tctcccgttt ttgaaaccgt ttcttccggc gcaccccatc 60  
 ctgaatgaat cagggtaaat tcggtttttt ctgcagaaaag ctcttttcaat tcaaattgtga 120  
 cgatccatcc cgacgtatcc cagctgaaaag cgagtcgatg cggcgcatca agctcgatca 180  
 ctttgcacgg ggagggggccg aaaggagact gcagggtgaa ttcgcagccg atctccgggc 240  
 ggaaatcatt aggcataaac caggcggcga tgccttcact ggtggcgacg gcctcccaca 300  
 ctttttctat cgatgcgtga aaaacagcct gtttatgtat atcaggcact agttgattgc 360  
 tcataataga cctcctagaa aaaagtaaaa ccaaattggtt tcctttctat tatatgaaac 420  
 ctttttagttt tatgtcaatg ttccgtcata attccctggg acaaggcata tcattgaaca 480  
 aacgaacctg aatgtaaagg atgaggggtt atg agt cat aga gca gat gag att 533  
 Met Ser His Arg Ala Asp Glu Ile  
 1 5  
 cga aaa aga atg gcc agg aaa aga aag cgg aaa aca ccg gac aaa cag 581  
 Arg Lys Arg Met Ala Arg Lys Arg Lys Arg Lys Thr Pro Asp Lys Gln  
 10 15 20  
 ccc ttt tca tca gac ggc aaa aag cgg ccg ctc aag ccg cct gca tgg 629  
 Pro Phe Ser Ser Asp Gly Lys Lys Arg Pro Leu Lys Pro Pro Ala Trp  
 25 30 35 40  
 aca gcc ttt tcg gaa gat gaa aaa gga gga gac ttc cct ccg cct gaa 677  
 Thr Ala Phe Ser Glu Asp Glu Lys Gly Gly Asp Phe Pro Pro Pro Glu  
 45 50 55  
 gga agt tcc ctg ctg ata aac ggg aag cac ccg ctt gtc aag gcg gat 725  
 Gly Ser Ser Leu Leu Ile Asn Gly Lys His Pro Leu Val Lys Ala Asp  
 60 65 70  
 gcg ctc atc ttg aaa tgt ctt ctg tcg gca tgc ctt gtt ctt gtg tcc 773  
 Ala Leu Ile Leu Lys Cys Leu Leu Ser Ala Cys Leu Val Leu Val Ser  
 75 80 85

gcc att gcc tac aaa ggc cag ttt gaa ccc gca aac caa atc aaa ccg Ala Ile Ala Tyr Lys Gly Gln Phe Glu Pro Ala Asn Gln Ile Lys Pro 90 95 100	821
gtt atc agc cag gtg ttt act gaa gag ttc caa ttt gcg gcc ctc cag Val Ile Ser Gln Val Phe Thr Glu Glu Phe Gln Phe Ala Ala Leu Gln 105 110 115 120	869
aat tgg tat gaa tcc aag ttc ggc gat ccc ctc gca ttc ttt cag ccg Asn Trp Tyr Glu Ser Lys Phe Gly Asp Pro Leu Ala Phe Phe Gln Pro 125 130 135	917
aaa ggc gcc aaa ccg tcc ggc cag gtc gag gtg aat cag gat ctc gct Lys Gly Ala Lys Pro Ser Gly Gln Val Glu Val Asn Gln Asp Leu Ala 140 145 150	965
gta cct gcc gta gga aag gtt cag gag aaa ttc tca ggg cag gcc att Val Pro Ala Val Gly Lys Val Gln Glu Lys Phe Ser Gly Gln Gly Ile 155 160 165	1013
aag gta gaa aca gaa gac gaa acg atc cgc agc atg aag gaa ggc tat Lys Val Glu Thr Glu Asp Glu Thr Ile Arg Ser Met Lys Glu Gly Tyr 170 175 180	1061
gtc att gaa gtg gac aaa aat ccg gaa aca ggc ctg acg gtg gtc ttg Val Ile Glu Val Asp Lys Asn Pro Glu Thr Gly Leu Thr Val Val Leu 185 190 195 200	1109
cag cat gcg gac aac agc tat acc tac tac ggc cag ctg aaa aaa gcg Gln His Ala Asp Asn Ser Tyr Thr Tyr Tyr Gly Gln Leu Lys Lys Ala 205 210 215	1157
gat gtc gct tta tac gat tat ata gat aaa gga acg aag ctc gga acg Asp Val Ala Leu Tyr Asp Tyr Ile Asp Lys Gly Thr Lys Leu Gly Thr 220 225 230	1205
att gag cag gat aaa aat caa aaa ggc atc tat tac ttt gcg atc aaa Ile Glu Gln Asp Lys Asn Gln Lys Gly Ile Tyr Tyr Phe Ala Ile Lys 235 240 245	1253
caa gga gag gaa ttt gtt gat ccg ata cag gtg atc aca ttt gag Gln Gly Glu Glu Phe Val Asp Pro Ile Gln Val Ile Thr Phe Glu 250 255 260	1298
taa atggacg gagctcttca ccaagcttca cattcatccg ctgctgtggc ttgtcatggc 1358	
gatcggatc atgacaggac atattaaagg cgcgtgtttt gtttaatgca cccaggaag 1417	

<210> 79  
 <211> 263  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 79

Met Ser His Arg Ala Asp Glu Ile Arg Lys Arg Met Ala Arg Lys Arg

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Lys Arg Lys Thr Pro Asp Lys Gln Pro Phe Ser Ser Asp Gly Lys Lys	20	25	30
Arg Pro Leu Lys Pro Pro Ala Trp Thr Ala Phe Ser Glu Asp Glu Lys	35	40	45
Gly Gly Asp Phe Pro Pro Pro Glu Gly Ser Ser Leu Leu Ile Asn Gly	50	55	60
Lys His Pro Leu Val Lys Ala Asp Ala Leu Ile Leu Lys Cys Leu Leu	65	70	75
Ser Ala Cys Leu Val Leu Val Ser Ala Ile Ala Tyr Lys Gly Gln Phe	85	90	95
Glu Pro Ala Asn Gln Ile Lys Pro Val Ile Ser Gln Val Phe Thr Glu	100	105	110
Glu Phe Gln Phe Ala Ala Leu Gln Asn Trp Tyr Glu Ser Lys Phe Gly	115	120	125
Asp Pro Leu Ala Phe Phe Gln Pro Lys Gly Ala Lys Pro Ser Gly Gln	130	135	140
Val Glu Val Asn Gln Asp Leu Ala Val Pro Ala Val Gly Lys Val Gln	145	150	155
Glu Lys Phe Ser Gly Gln Gly Ile Lys Val Glu Thr Glu Asp Glu Thr	165	170	175
Ile Arg Ser Met Lys Glu Gly Tyr Val Ile Glu Val Asp Lys Asn Pro	180	185	190
Glu Thr Gly Leu Thr Val Val Leu Gln His Ala Asp Asn Ser Tyr Thr	195	200	205
Tyr Tyr Gly Gln Leu Lys Lys Ala Asp Val Ala Leu Tyr Asp Tyr Ile	210	215	220
Asp Lys Gly Thr Lys Leu Gly Thr Ile Glu Gln Asp Lys Asn Gln Lys	225	230	235
			240



Gly Ile Tyr Tyr Phe Ala Ile Lys Gln Gly Glu Glu Phe Val Asp Pro  
245 250 255

Ile Gln Val Ile Thr Phe Glu  
260

<210> 80  
<211> 1468  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (982) .. (1428)

<400> 80  
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tatttatcag gtcagcaaag cggatcaaag catggtggtg ctggacgtga tgaaggtgat 120  
tgaagctgta cataaatcgt ttcttgacct tgatgtccaa accgtcggcg gttctgaaac 180  
catcgtggag atccaatattc cgaaaaggga tctgtcgccc gtgcttttca tcgccgtctg 240  
gctgctcttg ttcgtcggtg ccggccttgc cgtcatgaac tttcatgaag atgtcagcat 300  
gaggggaagtg cacatcctgc tttacgaaat ggtgacgggc aaggtgaacc gctatccata 360  
cctttttgcag gttccgtaca gcatcgggtct tggcctcggc atgatcttgt tttttaatca 420  
tttattttaa aaacgggtta acgaggagcc cagccccctg gaggtcgaga tgtttaaata 480  
tcagcttgat ttggaccatt atgtggccat gcacgaaaac aaagaaacga caaaggatat 540  
tcatgatcat tagcgtgata tttatcatct ttctcggact cgcaggaggg gttgctgttg 600  
gatccggctt tgtcgctttt cttaccgtgc ttggcattat cccgaggctg actcagctga 660  
cgaaaacaaa aggatttatc caggcgtatg aatgggctgt catttttaggc gcggttttcg 720  
gaggatggga atcgctgaac atgtcccgtt tttttttatc caaatggctg cttgttccga 780  
tcggcctttt tgcgggcgtt ttcattggaa tgcttgacgc ggcgctaaca gaagtcttga 840  
acgtgctgcc gatactggcg aaacgcatcg ggatgggaga ccggattttg atacttttaa 900  
tggccattgt tttcggcaag attctcggat cgatgttcca atggctcatt tttgttcatt 960  
tgtcataaaa ggaggattat g atg tca agt ttg aaa gat aat tat caa tcg 1011  
Met Ser Ser Leu Lys Asp Asn Tyr Gln Ser  
1 5 10

aaa gtt aaa gcg tat cag cct tca ccg cct tat gtc ctg aac tgt atc	1059
Lys Val Lys Ala Tyr Gln Pro Ser Pro Pro Tyr Val Leu Asn Cys Ile	
15 20 25	
aag gca ttt ctc gtc ggt ggt ctg att tgt acg atc ggc cag gct ttc	1107
Lys Ala Phe Leu Val Gly Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe	
30 35 40	
cag aat ttt tat atg gct gtg ttc cat ttt gat gaa aaa acg gcc ggg	1155
Gln Asn Phe Tyr Met Ala Val Phe His Phe Asp Glu Lys Thr Ala Gly	
45 50 55	
aac ccg acg gtt gcc acg ctg atc ctg atc tcc gct ctg tta aca ggc	1203
Asn Pro Thr Val Ala Thr Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly	
60 65 70	
ctt ggc gtc tac gac aga atc gga cag ttt gcc ggc gct ggt tct gcc	1251
Leu Gly Val Tyr Asp Arg Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala	
75 80 85 90	
gtt ccg gtt aca ggg ttt gcc aac agt atg acg agc gca gcg ctg gag	1299
Val Pro Val Thr Gly Phe Ala Asn Ser Met Thr Ser Ala Ala Leu Glu	
95 100 105	
cat aaa agc gaa agc tac gtc ctc ggc gta tgg aca aac atg ttc aag	1347
His Lys Ser Glu Ser Tyr Val Leu Gly Val Trp Thr Asn Met Phe Lys	
110 115 120	
ctt gcg gga aac gtc atc gtg ttc ggt gtt gtg gcc gct tat att gtg	1395
Leu Ala Gly Asn Val Ile Val Phe Gly Val Val Ala Ala Tyr Ile Val	
125 130 135	
ggg atg atc cgc ttt gcc ttt gac aag ctg ttt taggaggaaa acatcatgaa	1448
Gly Met Ile Arg Phe Ala Phe Asp Lys Leu Phe	
140 145	
attaacagga aaacaaacat	1468

<210> 81  
 <211> 149  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 81

Met Ser Ser Leu Lys Asp Asn Tyr Gln Ser Lys Val Lys Ala Tyr Gln
1 5 10 15

Pro Ser Pro Pro Tyr Val Leu Asn Cys Ile Lys Ala Phe Leu Val Gly
20 25 30

Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe Gln Asn Phe Tyr Met Ala
35 40 45

Val Phe His Phe Asp Glu Lys Thr Ala Gly Asn Pro Thr Val Ala Thr  
 50 55 60

Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly Leu Gly Val Tyr Asp Arg  
 65 70 75 80

Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala Val Pro Val Thr Gly Phe  
 85 90 95

Ala Asn Ser Met Thr Ser Ala Ala Leu Glu His Lys Ser Glu Ser Tyr  
 100 105 110

Val Leu Gly Val Trp Thr Asn Met Phe Lys Leu Ala Gly Asn Val Ile  
 115 120 125

Val Phe Gly Val Val Ala Ala Tyr Ile Val Gly Met Ile Arg Phe Ala  
 130 135 140

Phe Asp Lys Leu Phe  
 145

<210> 82  
 <211> 1453  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (504) .. (950)

<400> 82  
 tatcagcttg atttggacca ttatgtggcc atgcacgaaa acaaagaaac gacaaaggat 60  
 attcatgatac attagcgtga tatttatcat ctttctcgga ctgcgaggag gggttgctgt 120  
 tggatccggc tttgtcgctt ttcttaccgt gcttggcatt atcccagggc tgactcagct 180  
 gacgaaaaca aaaggattta tccaggcgta tgaatgggct gtcatttttag gcgcgggttt 240  
 cggaggatgg gaatcgctga acatgtcccg ctttttttta tccaaatggc tgcttggtcc 300  
 gatcggcctt tttgcgggcg ttttcattgg aatgcttgca gcggcgctaa cagaagtctt 360  
 gaacgtgctg ccgatactgg cgaaacgcat cgggatggga gaccggattt tgatactttt 420  
 aatggccatt gttttcggca agattctcgg atcgatgttc caatggctca tttttgttca 480  
 tttgtcataa aaggaggatt atg atg tca agt ttg aaa gat aat tat caa tcg 533

	Met	Ser	Ser	Leu	Lys	Asp	Asn	Tyr	Gln	Ser	
	1				5					10	
aaa gtt aaa gcg tat cag cct tca ccg cct tat gtc ctg aac tgt atc											581
Lys Val Lys Ala Tyr Gln Pro Ser Pro Pro Tyr Val Leu Asn Cys Ile											
	15				20				25		
aag gca ttt ctc gtc ggt ggt ctg att tgt acg atc ggc cag gct ttc											629
Lys Ala Phe Leu Val Gly Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe											
	30				35				40		
cag aat ttt tat atg gct gtg ttc cat ttt gat gaa aaa acg gcc ggg											677
Gln Asn Phe Tyr Met Ala Val Phe His Phe Asp Glu Lys Thr Ala Gly											
	45				50				55		
aac ccg acg gtt gcc acg ctg atc ctg atc tcc gct ctg tta aca ggc											725
Asn Pro Thr Val Ala Thr Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly											
	60				65				70		
ctt ggc gtc tac gac aga atc gga cag ttt gcc ggc gct ggt tct gcc											773
Leu Gly Val Tyr Asp Arg Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala											
	75				80				85		90
gtt ccg gtt aca ggg ttt gcc aac agt atg acg agc gca gcg ctg gag											821
Val Pro Val Thr Gly Phe Ala Asn Ser Met Thr Ser Ala Ala Leu Glu											
	95				100				105		
cat aaa agc gaa agc tac gtc ctc ggc gta tgg aca aac atg ttc aag											869
His Lys Ser Glu Ser Tyr Val Leu Gly Val Trp Thr Asn Met Phe Lys											
	110				115				120		
ctt gcg gga aac gtc atc gtg ttc ggt gtt gtg gcc gct tat att gtg											917
Leu Ala Gly Asn Val Ile Val Phe Gly Val Val Ala Ala Tyr Ile Val											
	125				130				135		
ggg atg atc cgc ttt gcc ttt gac aag ctg ttt taggaggaaa acatcatgaa											970
Gly Met Ile Arg Phe Ala Phe Asp Lys Leu Phe											
	140				145						
attaacagga aaacaaacat gggaattcga gaacccgctg tttgttaact caagcggaa											1030
agcgggtcgggt cccaaagaaa aagaaggtcc tcttggacac ttatttgaca aaagctatga											1090
tgaaatgcac tgcaaccaga aaaactggga aatggcagag cgcaagctga tggaggatgc											1150
ggttcagtcg gcgttatcaa aacaaaatct taaaaaggaa gacatcgata tctttttggc											1210
tggcgatctg ctcaacaaaa acgtgacagc caactatgtg gcgcggcatt tgaaaattcc											1270
ttttctctgc ttatttgag catgctcgac atcaatggaa tcgatcgca tcagttcggc											1330
gttgattgac ggggggtttcg caaagcgcgc cctagcggca accagcagcc ataatgctac											1390
ggcagaaaagg cagttccgct acccgacgga atacgggggg caaaaaccgg gaaccgcgac											1450
ttc											1453

<210> 83  
 <211> 149  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 83

Met Ser Ser Leu Lys Asp Asn Tyr Gln Ser Lys Val Lys Ala Tyr Gln  
 1 5 10 15

Pro Ser Pro Pro Tyr Val Leu Asn Cys Ile Lys Ala Phe Leu Val Gly  
 20 25 30

Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe Gln Asn Phe Tyr Met Ala  
 35 40 45

Val Phe His Phe Asp Glu Lys Thr Ala Gly Asn Pro Thr Val Ala Thr  
 50 55 60

Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly Leu Gly Val Tyr Asp Arg  
 65 70 75 80

Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala Val Pro Val Thr Gly Phe  
 85 90 95

Ala Asn Ser Met Thr Ser Ala Ala Leu Glu His Lys Ser Glu Ser Tyr  
 100 105 110

Val Leu Gly Val Trp Thr Asn Met Phe Lys Leu Ala Gly Asn Val Ile  
 115 120 125

Val Phe Gly Val Val Ala Ala Tyr Ile Val Gly Met Ile Arg Phe Ala  
 130 135 140

Phe Asp Lys Leu Phe  
 145

<210> 84  
 <211> 2020  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501) .. (1517)

<400> 84  
gctcattttt gttcatttgt cataaaaagga ggattatgat gtcaagtttg aaagataatt 60  
atcaatcgaa agttaagcg tatcagcctt caccgcctta tgtcctgaac tgtatcaagg 120  
catttctcgt cggtaggtctg atttgtacga tcggccaggc tttccagaat ttttatatgg 180  
ctgtgttcca ttttgatgaa aaaacggccg ggaacccgac ggttgccacg ctgatcctga 240  
tctccgctct gttaacaggc cttggcgtct acgacagaat cggacagttt gccggcgctg 300  
gttctgccgt tccggttaca gggtttgcca acagtatgac gagcgcagcg ctggagcata 360  
aaagcgaaaag ctacgtcctc ggcgatatgga caaacatgtt caagcttgcg ggaaacgtca 420  
tcgtgttcgg tgttgtggcc gcttatattg tggggatgat ccgctttgcc tttgacaagc 480  
tggttttagga ggaaaaacatc atg aaa tta aca gga aaa caa aca tgg gaa ttc 533  
Met Lys Leu Thr Gly Lys Gln Thr Trp Glu Phe  
1 5 10  
gag aac ccg ctg ttt gtt aac tca agc gga aca gcg gtc ggt ccc aaa 581  
Glu Asn Pro Leu Phe Val Asn Ser Ser Gly Thr Ala Val Gly Pro Lys  
15 20 25  
gaa aaa gaa ggt cct ctt gga cac tta ttt gac aaa agc tat gat gaa 629  
Glu Lys Glu Gly Pro Leu Gly His Leu Phe Asp Lys Ser Tyr Asp Glu  
30 35 40  
atg cac tgc aac cag aaa aac tgg gaa atg gca gag cgc aag ctg atg 677  
Met His Cys Asn Gln Lys Asn Trp Glu Met Ala Glu Arg Lys Leu Met  
45 50 55  
gag gat gcg gtt cag tcc gcg tta tca aaa caa aat ctt aaa aag gaa 725  
Glu Asp Ala Val Gln Ser Ala Leu Ser Lys Gln Asn Leu Lys Lys Glu  
60 65 70 75  
gac atc gat atc ttt ttg gct ggc gat ctg ctc aac caa aac gtg aca 773  
Asp Ile Asp Ile Phe Leu Ala Gly Asp Leu Leu Asn Gln Asn Val Thr  
80 85 90  
gcc aac tat gtg gcg cgg cat ttg aaa att cct ttt ctc tgc tta ttt 821  
Ala Asn Tyr Val Ala Arg His Leu Lys Ile Pro Phe Leu Cys Leu Phe  
95 100 105  
gga gca tgc tcg aca tca atg gaa tcg atc gcg atc agt tcg gcg ttg 869  
Gly Ala Cys Ser Thr Ser Met Glu Ser Ile Ala Ile Ser Ser Ala Leu  
110 115 120  
att gac ggg ggt ttc gca aag cgc gcc cta gcg gca acc agc agc cat 917  
Ile Asp Gly Gly Phe Ala Lys Arg Ala Leu Ala Ala Thr Ser Ser His  
125 130 135  
aat gct acg gca gaa agg cag ttc cgc tac ccg acg gaa tac ggg ggg 965  
Asn Ala Thr Ala Glu Arg Gln Phe Arg Tyr Pro Thr Glu Tyr Gly Gly  
140 145 150 155

caa aaa ccg gga acc gcg act tcg aca gtg acc gga agc gga gcg gtc Gln Lys Pro Gly Thr Ala Thr Ser Thr Val Thr Gly Ser Gly Ala Val 160 165 170	1013
gtc ctc agc cag cag ccc ggc gga att aaa att aca agc gca act gtc Val Leu Ser Gln Gln Pro Gly Gly Ile Lys Ile Thr Ser Ala Thr Val 175 180 185	1061
gga agg gtt atc gac ttg ggg att acc gat tcg caa gat atg ggg tcg Gly Arg Val Ile Asp Leu Gly Ile Thr Asp Ser Gln Asp Met Gly Ser 190 195 200	1109
gcg atg gca ccc gct gct gcg gat acg atc aag cag cat ttg gag gat Ala Met Ala Pro Ala Ala Ala Asp Thr Ile Lys Gln His Leu Glu Asp 205 210 215	1157
ctg gga cgc acc cct gat gat tac gat ctg atc tta acc ggc gac ctt Leu Gly Arg Thr Pro Asp Asp Tyr Asp Leu Ile Leu Thr Gly Asp Leu 220 225 230 235	1205
tca ggc gtc ggc agc ccg att ttg aag gat ctg tta aaa gag gaa gga Ser Gly Val Gly Ser Pro Ile Leu Lys Asp Leu Leu Lys Glu Glu Gly 240 245 250	1253
atc aat gtc ggg aca aaa cat aat gac tgc ggc ctg atg atc tat acg Ile Asn Val Gly Thr Lys His Asn Asp Cys Gly Leu Met Ile Tyr Thr 255 260 265	1301
cct gac cag caa gtt ttt gca ggt gga agc gga tgc gct tgt tcc gcg Pro Asp Gln Gln Val Phe Ala Gly Gly Ser Gly Cys Ala Cys Ser Ala 270 275 280	1349
gtc gtc acc ttt gcc cat att ttc aaa gaa att gaa gcg gga agg ctg Val Val Thr Phe Ala His Ile Phe Lys Glu Ile Glu Ala Gly Arg Leu 285 290 295	1397
aac aga gtg ctt gtt gtc gcg aca ggc gcc ctt tta agc ccg acg atc Asn Arg Val Leu Val Val Ala Thr Gly Ala Leu Leu Ser Pro Thr Ile 300 305 310 315	1445
atc cag caa aaa gaa tcg ata cca tgc att gcc cat ggc gtc gta ttt Ile Gln Gln Lys Glu Ser Ile Pro Cys Ile Ala His Gly Val Val Phe 320 325 330	1493
gaa cgg gcc gaa agg ggg aac gct taagatggag tatgtcattg cttttattgc Glu Arg Ala Glu Arg Gly Asn Ala 335	1547
aggcgggctg atttgctca tcggacagct cttgcttgat atcttcaaaa tgacgccggc	1607
tcatgtcatg tcaacttttg tcgtatctgg agcgatcctt gacggattcg gcatttacga	1667
ccgttttatc gaatttgccg gtgccggggc tacagtcccg attgtcagct tcggccactc	1727
tcttttgcac ggcgcgatgc accaggctga gaaacatggc tttatcggaa tcggcatggg	1787

gatatttgaa ctgacatctg ccggtatatc tgccgctatc ttgttcgctt ttcttgttgc 1847  
 cgtgattttt aaaccgaaag gataaaggaa aatgccagca aaacgcaagg tcatttttgg 1907  
 cacagacggc gatataatcg ctgcaaaagc aatcgaatat gcagcaagaa aaacgggtgg 1967  
 ccgctgcatt tccaatcgg cggggaatcc gagcgtaaaa acaggaccgg agc 2020

<210> 85  
 <211> 339  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 85

Met Lys Leu Thr Gly Lys Gln Thr Trp Glu Phe Glu Asn Pro Leu Phe  
 1 5 10 15

Val Asn Ser Ser Gly Thr Ala Val Gly Pro Lys Glu Lys Glu Gly Pro  
 20 25 30

Leu Gly His Leu Phe Asp Lys Ser Tyr Asp Glu Met His Cys Asn Gln  
 35 40 45

Lys Asn Trp Glu Met Ala Glu Arg Lys Leu Met Glu Asp Ala Val Gln  
 50 55 60

Ser Ala Leu Ser Lys Gln Asn Leu Lys Lys Glu Asp Ile Asp Ile Phe  
 65 70 75 80

Leu Ala Gly Asp Leu Leu Asn Gln Asn Val Thr Ala Asn Tyr Val Ala  
 85 90 95

Arg His Leu Lys Ile Pro Phe Leu Cys Leu Phe Gly Ala Cys Ser Thr  
 100 105 110

Ser Met Glu Ser Ile Ala Ile Ser Ser Ala Leu Ile Asp Gly Gly Phe  
 115 120 125

Ala Lys Arg Ala Leu Ala Ala Thr Ser Ser His Asn Ala Thr Ala Glu  
 130 135 140

Arg Gln Phe Arg Tyr Pro Thr Glu Tyr Gly Gly Gln Lys Pro Gly Thr  
 145 150 155 160

Ala Thr Ser Thr Val Thr Gly Ser Gly Ala Val Val Leu Ser Gln Gln



165	170	175
Pro Gly Gly Ile Lys Ile Thr Ser Ala Thr Val Gly Arg Val Ile Asp		
180	185	190
Leu Gly Ile Thr Asp Ser Gln Asp Met Gly Ser Ala Met Ala Pro Ala		
195	200	205
Ala Ala Asp Thr Ile Lys Gln His Leu Glu Asp Leu Gly Arg Thr Pro		
210	215	220
Asp Asp Tyr Asp Leu Ile Leu Thr Gly Asp Leu Ser Gly Val Gly Ser		
225	230	235 240
Pro Ile Leu Lys Asp Leu Leu Lys Glu Glu Gly Ile Asn Val Gly Thr		
245	250	255
Lys His Asn Asp Cys Gly Leu Met Ile Tyr Thr Pro Asp Gln Gln Val		
260	265	270
Phe Ala Gly Gly Ser Gly Cys Ala Cys Ser Ala Val Val Thr Phe Ala		
275	280	285
His Ile Phe Lys Glu Ile Glu Ala Gly Arg Leu Asn Arg Val Leu Val		
290	295	300
Val Ala Thr Gly Ala Leu Leu Ser Pro Thr Ile Ile Gln Gln Lys Glu		
305	310	315 320
Ser Ile Pro Cys Ile Ala His Gly Val Val Phe Glu Arg Ala Glu Arg		
325	330	335

Gly Asn Ala

<210> 86  
 <211> 2473  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501) .. (1970)

<400> 86  
cgaatatgca gcaagaaaaa cgggtggccg ctgcatttcc caatcggcgg ggaatccgag 60  
cgtaaaca ggaccggagc ttgtaaccat gatcctgcaa acccctcatg atcctgtatt 120  
cgtcatgttt gatgattccg gacttcaagg tgaaggcccg ggagagacag ctatgaaata 180  
tgtagcgatg catcccgata tcgaggtgct cggagtcac gccgtcgctt caaaaactca 240  
ttatgcagag tggacgagag tcgatgtatc aatcgatgca gaaggcgaac tgacagagta 300  
cggcgtcgat aaacacgggg tcaaagagtt cgatgtcaaa cgaatgaatg gtgatacagt 360  
ctattgcctt gaccagctgg atgttccgat cattgtcggga atcgggtgata tcggtaagat 420  
gaacagaaaa gacgatgtgg aaaaagggtt gccgattaca atgaaagcgg tcgagctcat 480  
tttagaaagg agcgggtatc atg agt gct caa aag caa gag aag acg aac gta 533  
Met Ser Ala Gln Lys Gln Glu Lys Thr Asn Val  
1 5 10  
ttc ctt gat cct tct aag aat gaa gcg tat ttc aag aag cgg gtc ggc 581  
Phe Leu Asp Pro Ser Lys Asn Glu Ala Tyr Phe Lys Lys Arg Val Gly  
15 20 25  
atg gga gaa agc ttt gac ctt ggc gta cgg aag gtc ttt att ctc gga 629  
Met Gly Glu Ser Phe Asp Leu Gly Val Arg Lys Val Phe Ile Leu Gly  
30 35 40  
cat gaa gtt cag ctt tat tat gtc aac gga ttg tgc gac aca caa tac 677  
His Glu Val Gln Leu Tyr Tyr Val Asn Gly Leu Cys Asp Thr Gln Tyr  
45 50 55  
atc att cac ctg tta aga gaa ctg gtg cat ctg aat gat aaa gaa aaa 725  
Ile Ile His Leu Leu Arg Glu Leu Val His Leu Asn Asp Lys Glu Lys  
60 65 70 75  
gaa tcg ggc gag gtc gaa gac atc gtc gaa aac agg ctt ttg aac cag 773  
Glu Ser Gly Glu Val Glu Asp Ile Val Glu Asn Arg Leu Leu Asn Gln  
80 85 90  
cag gtt tca aaa gcg gaa acg ctt gat gaa gct gtc gac caa gtg ttg 821  
Gln Val Ser Lys Ala Glu Thr Leu Asp Glu Ala Val Asp Gln Val Leu  
95 100 105  
tca gga ctg gtt gcc atc atc gtc gaa gat gcg ggc ttt gct ttt atc 869  
Ser Gly Leu Val Ala Ile Ile Val Glu Asp Ala Gly Phe Ala Phe Ile  
110 115 120  
atc gat gtc aga agc tac ccg ggc aga acg ccg gaa gaa cct gat aca 917  
Ile Asp Val Arg Ser Tyr Pro Gly Arg Thr Pro Glu Glu Pro Asp Thr  
125 130 135  
gaa aaa gtc gta cgc ggt gca agg gac gga ctc gtc gag aac atc atc 965  
Glu Lys Val Val Arg Gly Ala Arg Asp Gly Leu Val Glu Asn Ile Ile  
140 145 150 155

gtc aac aca gcc ctg att aga cgc cgg atc aga gat gag cgc ttg cgc	1013
Val Asn Thr Ala Leu Ile Arg Arg Arg Ile Arg Asp Glu Arg Leu Arg	
160 165 170	
tac aaa atg ctt cat atc ggt gaa cgc tct aaa aca gac atc tgc ctc	1061
Tyr Lys Met Leu His Ile Gly Glu Arg Ser Lys Thr Asp Ile Cys Leu	
175 180 185	
tgc tat ttg gaa gac gtt gca gat ccc gat ctt gtt gaa gta tta aaa	1109
Cys Tyr Leu Glu Asp Val Ala Asp Pro Asp Leu Val Glu Val Leu Lys	
190 195 200	
aaa gaa att gaa gat gtg aag atc gac ggg ctg ccg atg tcg gat aaa	1157
Lys Glu Ile Glu Asp Val Lys Ile Asp Gly Leu Pro Met Ser Asp Lys	
205 210 215	
tcg gta gag gaa ttc ctg gtc ggc caa ggc tac aat ccg ttt ccg ctt	1205
Ser Val Glu Glu Phe Leu Val Gly Gln Gly Tyr Asn Pro Phe Pro Leu	
220 225 230 235	
gtc agg ttt acg gaa agg gca gac gta gcc gca agc cat att tta gag	1253
Val Arg Phe Thr Glu Arg Ala Asp Val Ala Ala Ser His Ile Leu Glu	
240 245 250	
ggg cat gtc atc gtg atc gtc gat acg tcg cca agc gtc atc atc aca	1301
Gly His Val Ile Val Ile Val Asp Thr Ser Pro Ser Val Ile Ile Thr	
255 260 265	
ccg acc act ttg ttt cac cat gtt cag cat gct gag gaa tac aga cag	1349
Pro Thr Thr Leu Phe His His Val Gln His Ala Glu Glu Tyr Arg Gln	
270 275 280	
acg ccg gct gtt ggg acg ttt tta agg tgg gtg ccg ttt ttc ggt att	1397
Thr Pro Ala Val Gly Thr Phe Leu Arg Trp Val Arg Phe Phe Gly Ile	
285 290 295	
ttg gcc tcc acc ttt ttg ctg ccg ctt tgg ctg ctg ttt gtc att cat	1445
Leu Ala Ser Thr Phe Leu Leu Pro Leu Trp Leu Leu Phe Val Ile His	
300 305 310 315	
ccg tcg ctc ttg cct gat aat tta tcg ttt atc ggg ttg aat aaa gac	1493
Pro Ser Leu Leu Pro Asp Asn Leu Ser Phe Ile Gly Leu Asn Lys Asp	
320 325 330	
acc cat att ccg att atc atg cag att ttc ctg gcg gat ctc ggc gtc	1541
Thr His Ile Pro Ile Ile Met Gln Ile Phe Leu Ala Asp Leu Gly Val	
335 340 345	
gaa ttt tta aga atg gcc gcc att cat acg ccg acg gcg ctt tcg act	1589
Glu Phe Leu Arg Met Ala Ala Ile His Thr Pro Thr Ala Leu Ser Thr	
350 355 360	
gca atg ggc ctg atc gcc gct gta ttg atc ggc gat atc gcg atc aat	1637
Ala Met Gly Leu Ile Ala Ala Val Leu Ile Gly Asp Ile Ala Ile Asn	
365 370 375	
gtc ggc ttg ttt tct ccc gaa gtc att tta tac gtt tcc ctc tcg gca	1685



Lys Asn Glu Ala Tyr Phe Lys Lys Arg Val Gly Met Gly Glu Ser Phe  
 20 25 30

Asp Leu Gly Val Arg Lys Val Phe Ile Leu Gly His Glu Val Gln Leu  
 35 40 45

Tyr Tyr Val Asn Gly Leu Cys Asp Thr Gln Tyr Ile Ile His Leu Leu  
 50 55 60

Arg Glu Leu Val His Leu Asn Asp Lys Glu Lys Glu Ser Gly Glu Val  
 65 70 75 80

Glu Asp Ile Val Glu Asn Arg Leu Leu Asn Gln Gln Val Ser Lys Ala  
 85 90 95

Glu Thr Leu Asp Glu Ala Val Asp Gln Val Leu Ser Gly Leu Val Ala  
 100 105 110

Ile Ile Val Glu Asp Ala Gly Phe Ala Phe Ile Ile Asp Val Arg Ser  
 115 120 125

Tyr Pro Gly Arg Thr Pro Glu Glu Pro Asp Thr Glu Lys Val Val Arg  
 130 135 140

Gly Ala Arg Asp Gly Leu Val Glu Asn Ile Ile Val Asn Thr Ala Leu  
 145 150 155 160

Ile Arg Arg Arg Ile Arg Asp Glu Arg Leu Arg Tyr Lys Met Leu His  
 165 170 175

Ile Gly Glu Arg Ser Lys Thr Asp Ile Cys Leu Cys Tyr Leu Glu Asp  
 180 185 190

Val Ala Asp Pro Asp Leu Val Glu Val Leu Lys Lys Glu Ile Glu Asp  
 195 200 205

Val Lys Ile Asp Gly Leu Pro Met Ser Asp Lys Ser Val Glu Glu Phe  
 210 215 220

Leu Val Gly Gln Gly Tyr Asn Pro Phe Pro Leu Val Arg Phe Thr Glu  
 225 230 235 240

Arg Ala Asp Val Ala Ala Ser His Ile Leu Glu Gly His Val Ile Val

245					250					255					
Ile	Val	Asp	Thr	Ser	Pro	Ser	Val	Ile	Ile	Thr	Pro	Thr	Thr	Leu	Phe
			260					265					270		
His	His	Val	Gln	His	Ala	Glu	Glu	Tyr	Arg	Gln	Thr	Pro	Ala	Val	Gly
		275					280					285			
Thr	Phe	Leu	Arg	Trp	Val	Arg	Phe	Phe	Gly	Ile	Leu	Ala	Ser	Thr	Phe
	290					295					300				
Leu	Leu	Pro	Leu	Trp	Leu	Leu	Phe	Val	Ile	His	Pro	Ser	Leu	Leu	Pro
305					310					315					320
Asp	Asn	Leu	Ser	Phe	Ile	Gly	Leu	Asn	Lys	Asp	Thr	His	Ile	Pro	Ile
				325					330					335	
Ile	Met	Gln	Ile	Phe	Leu	Ala	Asp	Leu	Gly	Val	Glu	Phe	Leu	Arg	Met
		340						345					350		
Ala	Ala	Ile	His	Thr	Pro	Thr	Ala	Leu	Ser	Thr	Ala	Met	Gly	Leu	Ile
		355					360					365			
Ala	Ala	Val	Leu	Ile	Gly	Asp	Ile	Ala	Ile	Asn	Val	Gly	Leu	Phe	Ser
		370				375						380			
Pro	Glu	Val	Ile	Leu	Tyr	Val	Ser	Leu	Ser	Ala	Ile	Gly	Ala	Tyr	Thr
385					390					395					400
Thr	Pro	Ser	Tyr	Glu	Leu	Ser	Leu	Ala	Asn	Lys	Met	Val	Lys	Leu	Phe
				405					410					415	
Met	Leu	Ile	Leu	Val	Ala	Leu	Phe	Lys	Val	Glu	Gly	Phe	Val	Ile	Gly
			420					425					430		
Leu	Thr	Ile	Leu	Thr	Ile	Val	Met	Thr	Ser	Ile	Arg	Ser	Leu	Arg	Thr
		435					440					445			
Pro	Tyr	Leu	Trp	Pro	Leu	Leu	Pro	Phe	Asn	Gly	Lys	Ala	Phe	Trp	His
		450					455				460				
Val	Leu	Val	Arg	Thr	Ser	Val	Pro	Gly	Gly	Lys	Val	Arg	Pro	Ser	Ile
465					470					475					480

Val His Pro Arg Asn Arg Ser Arg Gln Pro  
485 490

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<211> 1567  
<212> DNA  
<213> Bacillus licheniformis

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<222> (501)..(1064)

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cagccgcttt acgagctgtc tgtcacagca aagccgaaga acattccgca gacgatcgag 180  
gttgatattt ccagtctcga agtcaatgat gttctaaccg tcggcgatat tccgacaaaa 240  
ggcgattatt catacaacca tgagcctgat gaagttgttg catccattct tcctcctcaa 300  
aagcaggaag aaacagaagc cgaatcagct gctcaagacg ttgaggaacc agaaaaaggc 360  
actgaagagg aaaaagaaga ataaatacgt aagacgtaat ccgcccgcgg ttacgtcttt 420  
tgtgctagaa tgaggggaaa ttaggatgct cccctcagt atgctgaggc aggggttttgc 480  
ttaagggagg atatagaata atg ctt gtg ttt gca gga ttg ggc aat ccg ggt 533  
Met Leu Val Phe Ala Gly Leu Gly Asn Pro Gly  
1 5 10  
aaa aca tat gaa aat acg aga cac aat gta ggt ttt atg acg att gac 581  
Lys Thr Tyr Glu Asn Thr Arg His Asn Val Gly Phe Met Thr Ile Asp  
15 20 25  
gag ctc tcg aaa gag tgg aac att ccg ctt gat aaa aca aag ttc aac 629  
Glu Leu Ser Lys Glu Trp Asn Ile Pro Leu Asp Lys Thr Lys Phe Asn  
30 35 40  
gga caa tac gga atc ggg ttt gtt tcc ggc aaa aag gtt cta ctt gtt 677  
Gly Gln Tyr Gly Ile Gly Phe Val Ser Gly Lys Lys Val Leu Leu Val  
45 50 55  
aag ccg ctt aca tat atg aat tta tcg gga gaa tgt ttg agg ccg ctt 725  
Lys Pro Leu Thr Tyr Met Asn Leu Ser Gly Glu Cys Leu Arg Pro Leu  
60 65 70 75  
ttg gac tat tac gag atc cct gtt gac aat ttg aaa gtg att tac gat 773  
Leu Asp Tyr Tyr Glu Ile Pro Val Asp Asn Leu Lys Val Ile Tyr Asp  
80 85 90

gat ttg gat ctt ccg acc gga aga atc cgt ctg agg acg aaa gga agc 821  
 Asp Leu Asp Leu Pro Thr Gly Arg Ile Arg Leu Arg Thr Lys Gly Ser  
                   95                                  100                                  105

gca gga ggc cat aac ggc atc aaa tcg acg att cag cat ctg gga aca 869  
 Ala Gly Gly His Asn Gly Ile Lys Ser Thr Ile Gln His Leu Gly Thr  
                   110                                  115                                  120

agt gag ttt aac cgg atc aga atc gga ata ggc cgt ccg gta aac ggc 917  
 Ser Glu Phe Asn Arg Ile Arg Ile Gly Ile Gly Arg Pro Val Asn Gly  
                   125                                  130                                  135

atg aaa gtc gtc gat tat gtg ctt ggc gct ttt aca gat gaa gaa gag 965  
 Met Lys Val Val Asp Tyr Val Leu Gly Ala Phe Thr Asp Glu Glu Glu  
                   140                                  145                                  150                                  155

ccg gcg ata aaa gag gcc gtc aga caa tcg gcc aag gcc tgt gaa gct 1013  
 Pro Ala Ile Lys Glu Ala Val Arg Gln Ser Ala Lys Ala Cys Glu Ala  
                                   160                                  165                                  170

tct ttg gaa aaa cct ttt tta gaa gtc atg aat gaa ttt aac gca aag 1061  
 Ser Leu Glu Lys Pro Phe Leu Glu Val Met Asn Glu Phe Asn Ala Lys  
                   175                                  180                                  185

gta taaggcaaaa gggaacggaa catactagtc ttaaaaagac tcggtatgga 1114  
 Val

ggttccttta tggctttaca ttattattgc cggcattgcg gcgttaaagt cggaagtctt 1174

gaccattctt atgtaaacag tgaacagtta ggctttaacc acttaacaaa tgatgaaaga 1234

aacgatatga tttcttatat ggataatggg gatttacacg tgaagacgat atgtgaagat 1294

tgtcaagaag cgcttgagcg aaaccggat tatcaccaat atcattcatt tattcaatag 1354

atagctttgg tgtagagact agaccaaagc atttttctat ttgaggaaga gaggaggggc 1414

tcatttgaac aatattcaat cctatataac aaaaagcgat gattttaaat ccatcgtcaa 1474

cggcttgaac gaagggctga aggaacagct gcttgcgggg ctctccggat ctgcccggtc 1534

gttatttaca gccgctctta caaaagaaac gag 1567

<210> 89

<211> 188

<212> PRT

<213> Bacillus licheniformis

<400> 89

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Thr Arg His Asn Val Gly Phe Met Thr Ile Asp Glu Leu Ser Lys Glu



20

25

30

Trp Asn Ile Pro Leu Asp Lys Thr Lys Phe Asn Gly Gln Tyr Gly Ile  
 35 40 45

Gly Phe Val Ser Gly Lys Lys Val Leu Leu Val Lys Pro Leu Thr Tyr  
 50 55 60

Met Asn Leu Ser Gly Glu Cys Leu Arg Pro Leu Leu Asp Tyr Tyr Glu  
 65 70 75 80

Ile Pro Val Asp Asn Leu Lys Val Ile Tyr Asp Asp Leu Asp Leu Pro  
 85 90 95

Thr Gly Arg Ile Arg Leu Arg Thr Lys Gly Ser Ala Gly Gly His Asn  
 100 105 110

Gly Ile Lys Ser Thr Ile Gln His Leu Gly Thr Ser Glu Phe Asn Arg  
 115 120 125

Ile Arg Ile Gly Ile Gly Arg Pro Val Asn Gly Met Lys Val Val Asp  
 130 135 140

Tyr Val Leu Gly Ala Phe Thr Asp Glu Glu Glu Pro Ala Ile Lys Glu  
 145 150 155 160

Ala Val Arg Gln Ser Ala Lys Ala Cys Glu Ala Ser Leu Glu Lys Pro  
 165 170 175

Phe Leu Glu Val Met Asn Glu Phe Asn Ala Lys Val  
 180 185

<210> 90

<211> 2097

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1598)

<400> 90

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gtccgccttt caaaagccgg tcattttgct ggcagggggg cttgaccgcg gaaatgaatt	180
tgatgaacta aagccgcata tgtcttttgt aaaagcgggtg atcacttttcg gcgagaccgc	240
gccgaagttt gagaagctgg ccgaagaaat gggaatacaa cagggttaaac gtgtcgataa	300
tgttgaacaa gcagcaactg cggcgttcag cctgtcagac gaaggagatg tcattcttct	360
gtccccggcc tgcgcaagct gggatcagta caaacattt gaagaacgtg gtgacatgtt	420
tgtaaacgcc gtgcatatgc ttaaataagg gcttgtctcg taaagatagc cctaagaatt	480
agagcttggg gtgttcggct ttg caa aca aaa aaa acg tca ccg gat ttt ttg	533
Leu Gln Thr Lys Lys Thr Ser Pro Asp Phe Leu	
1 5 10	
ctg gtt atc att acg cta ttg ctt tta aca atc gga ctg att atg gta	581
Leu Val Ile Ile Thr Leu Leu Leu Leu Thr Ile Gly Leu Ile Met Val	
15 20 25	
tac agc gcc agt gca gta tgg gcg act tac aaa tac gac gac tcc ttt	629
Tyr Ser Ala Ser Ala Val Trp Ala Thr Tyr Lys Tyr Asp Asp Ser Phe	
30 35 40	
ttc ttt gcg aaa cgg cag ctt ttg ttt gcc ggc atc ggg gtc atc gcc	677
Phe Phe Ala Lys Arg Gln Leu Leu Phe Ala Gly Ile Gly Val Ile Ala	
45 50 55	
atg ttt ttc atc atg aac gtc gac tac tgg acg tgg agg act tat gcg	725
Met Phe Phe Ile Met Asn Val Asp Tyr Trp Thr Trp Arg Thr Tyr Ala	
60 65 70 75	
aaa ata ctg atc att gta tgt ttc ttt ctg ctc atc atc gtc ctg gtt	773
Lys Ile Leu Ile Ile Val Cys Phe Phe Leu Leu Ile Ile Val Leu Val	
80 85 90	
ccc ggg atc ggc atg gaa cgg aac ggg tcg agg agc tgg atc gga gtc	821
Pro Gly Ile Gly Met Glu Arg Asn Gly Ser Arg Ser Trp Ile Gly Val	
95 100 105	
ggc gct ttc agc att cag ccg tcc gag ttt atg aaa ctc gcg atg atc	869
Gly Ala Phe Ser Ile Gln Pro Ser Glu Phe Met Lys Leu Ala Met Ile	
110 115 120	
gca ttt ttg gcc aag ttt tta tct gaa aag caa aag aat att acg tcg	917
Ala Phe Leu Ala Lys Phe Leu Ser Glu Lys Gln Lys Asn Ile Thr Ser	
125 130 135	
ttt aga aaa ggc ttt gtg ccg gcg ctg ggc att gtc ttt tca gct ttt	965
Phe Arg Lys Gly Phe Val Pro Ala Leu Gly Ile Val Phe Ser Ala Phe	
140 145 150 155	
ctg atc atc atg atg cag cct gac ctc gga aca gga acc gtg atg gtc	1013
Leu Ile Ile Met Met Gln Pro Asp Leu Gly Thr Gly Thr Val Met Val	
160 165 170	

ggc aca tgc atc att atg atc ttt gtc gcg ggg gcg aga att tcg cac	1061
Gly Thr Cys Ile Ile Met Ile Phe Val Ala Gly Ala Arg Ile Ser His	
175 180 185	
ttc gtt ttt ctc ggc ctg atc gga ctg agc ggt ttt gtc ggc ctt gtg	1109
Phe Val Phe Leu Gly Leu Ile Gly Leu Ser Gly Phe Val Gly Leu Val	
190 195 200	
ctg tcg gcg ccg tac cgg atc aaa agg atc act tca tac ttg aac cct	1157
Leu Ser Ala Pro Tyr Arg Ile Lys Arg Ile Thr Ser Tyr Leu Asn Pro	
205 210 215	
tgg gag gac cct tta gga agc ggc ttt caa atc att cag tct ctt tat	1205
Trp Glu Asp Pro Leu Gly Ser Gly Phe Gln Ile Ile Gln Ser Leu Tyr	
220 225 230 235	
gcg gtg ggg ccc ggc ggg ctg ttc ggc ctc ggc ctc ggc cag agc agg	1253
Ala Val Gly Pro Gly Gly Leu Phe Gly Leu Gly Leu Gly Gln Ser Arg	
240 245 250	
caa aag ttt ttc tat ctg cct gag ccg cag aca gat ttt att ttt gcg	1301
Gln Lys Phe Phe Tyr Leu Pro Glu Pro Gln Thr Asp Phe Ile Phe Ala	
255 260 265	
att tta tca gag gag ctc ggc ttt atc ggc gga tcg ctg att ctt ttg	1349
Ile Leu Ser Glu Glu Leu Gly Phe Ile Gly Gly Ser Leu Ile Leu Leu	
270 275 280	
ctc ttc agc gtt cta tta tgg aga ggc atc aga atc gcg ctc ggt gcg	1397
Leu Phe Ser Val Leu Leu Trp Arg Gly Ile Arg Ile Ala Leu Gly Ala	
285 290 295	
ccc gat tta tac ggc agt ttt gtc gcc gtc ggc gtc att tcg atg ata	1445
Pro Asp Leu Tyr Gly Ser Phe Val Ala Val Gly Val Ile Ser Met Ile	
300 305 310 315	
gcg att cag gtt atg atc aat atc gga gtc gtg act ggt ttg att cct	1493
Ala Ile Gln Val Met Ile Asn Ile Gly Val Val Thr Gly Leu Ile Pro	
320 325 330	
gtt aca ggc att acg ctt ccg ttt tta agc tat ggc ggt tca tca ctg	1541
Val Thr Gly Ile Thr Leu Pro Phe Leu Ser Tyr Gly Gly Ser Ser Leu	
335 340 345	
acc ttg atg ctc atg gcg gtc ggc gtg ctg ctg aat gtc agc agg tat	1589
Thr Leu Met Leu Met Ala Val Gly Val Leu Leu Asn Val Ser Arg Tyr	
350 355 360	
tct aga tac tagattttgg cgataaccct gttgcgagat agcagggtta	1638
Ser Arg Tyr	
365	
tcggcgtgta cataaggatt aagggggaga acagatgcgg attgttggtta gcggaggcgg	1698
aacggggcggc catattttacc ccgcccttgc gtttattaaa gaagtgaaac ggcattcacga	1758
agatgttgag tttttatata tcggaaccga aaaaggcctg gagaaaaata tcgtcgagcg	1818

ggaagggatc cctttcaaag cgattgaaat tacgggtttt aaaagaaaac tttcatttga 1878  
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 acgggttcaag ccggatgccg tgatcggcac gggcggctac gtgtgcggcc ccgtcgtata 1998  
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<210> 91  
 <211> 366  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 91

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Val Trp Ala Thr Tyr Lys Tyr Asp Asp Ser Phe Phe Phe Ala Lys Arg  
 35 40 45

Gln Leu Leu Phe Ala Gly Ile Gly Val Ile Ala Met Phe Phe Ile Met  
 50 55 60

Asn Val Asp Tyr Trp Thr Trp Arg Thr Tyr Ala Lys Ile Leu Ile Ile  
 65 70 75 80

Val Cys Phe Phe Leu Leu Ile Ile Val Leu Val Pro Gly Ile Gly Met  
 85 90 95

Glu Arg Asn Gly Ser Arg Ser Trp Ile Gly Val Gly Ala Phe Ser Ile  
 100 105 110

Gln Pro Ser Glu Phe Met Lys Leu Ala Met Ile Ala Phe Leu Ala Lys  
 115 120 125

Phe Leu Ser Glu Lys Gln Lys Asn Ile Thr Ser Phe Arg Lys Gly Phe  
 130 135 140

Val Pro Ala Leu Gly Ile Val Phe Ser Ala Phe Leu Ile Ile Met Met  
 145 150 155 160

Gln Pro Asp Leu Gly Thr Gly Thr Val Met Val Gly Thr Cys Ile Ile  
165 170 175

Met Ile Phe Val Ala Gly Ala Arg Ile Ser His Phe Val Phe Leu Gly  
180 185 190

Leu Ile Gly Leu Ser Gly Phe Val Gly Leu Val Leu Ser Ala Pro Tyr  
195 200 205

Arg Ile Lys Arg Ile Thr Ser Tyr Leu Asn Pro Trp Glu Asp Pro Leu  
210 215 220

Gly Ser Gly Phe Gln Ile Ile Gln Ser Leu Tyr Ala Val Gly Pro Gly  
225 230 235 240

Gly Leu Phe Gly Leu Gly Leu Gly Gln Ser Arg Gln Lys Phe Phe Tyr  
245 250 255

Leu Pro Glu Pro Gln Thr Asp Phe Ile Phe Ala Ile Leu Ser Glu Glu  
260 265 270

Leu Gly Phe Ile Gly Gly Ser Leu Ile Leu Leu Phe Ser Val Leu  
275 280 285

Leu Trp Arg Gly Ile Arg Ile Ala Leu Gly Ala Pro Asp Leu Tyr Gly  
290 295 300

Ser Phe Val Ala Val Gly Val Ile Ser Met Ile Ala Ile Gln Val Met  
305 310 315 320

Ile Asn Ile Gly Val Val Thr Gly Leu Ile Pro Val Thr Gly Ile Thr  
325 330 335

Leu Pro Phe Leu Ser Tyr Gly Gly Ser Ser Leu Thr Leu Met Leu Met  
340 345 350

Ala Val Gly Val Leu Leu Asn Val Ser Arg Tyr Ser Arg Tyr  
355 360 365

<210> 92  
<211> 1882  
<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1397)

<400> 92

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aaaagaaatc gttgatgtta agcggggccga acggctcggc gtactggggc agacggacct    180
tgagatcaat gagcaggacg gtcagattac cgctcttata atcccttctg ttaaattggtt    240
cggactagga agaaaacagg ggaatgacat taaggtgccc tggtcgcaaa ttcaaaaaat    300
cggctcggat atgatcattt tggatgttcc ggaaagcagc gtgacaaaag aggagtaagc    360
aaggtgaaaa cccgcccgtc ccatgggggc gggctttttg tttttctgga tttcaattca    420
ccgctatttc ctttttgtca tatgatgaaa ttagcttatg aattagatcc ttgtcaaaaa    480
agaaggtgaa tgttagagcc atg tta acc gga ttg acg att gca atc atc ggc      533
                Met Leu Thr Gly Leu Thr Ile Ala Ile Ile Gly
                  1             5             10

ggc gat gca agg cag ctc gag atc atc cgc aag ctg acg gaa cag gat      581
Gly Asp Ala Arg Gln Leu Glu Ile Ile Arg Lys Leu Thr Glu Gln Asp
                15             20             25

gca aag gtc ttt tta atc ggt ttt gat cag ctt gat cac ggg ttt acc      629
Ala Lys Val Phe Leu Ile Gly Phe Asp Gln Leu Asp His Gly Phe Thr
                30             35             40

gga gct aca aaa cta aag ctg aac gaa ctt gat ttt ggc aca ata gac      677
Gly Ala Thr Lys Leu Lys Leu Asn Glu Leu Asp Phe Gly Thr Ile Asp
                45             50             55

agc att att ctg cct gta tcg ggc aca tcg atg gaa gga acg gtt gcg      725
Ser Ile Ile Leu Pro Val Ser Gly Thr Ser Met Glu Gly Thr Val Ala
        60             65             70             75

act gtt ttt tcc aat gaa aaa gtg gtg tta aaa cag gaa cat tta gaa      773
Thr Val Phe Ser Asn Glu Lys Val Val Leu Lys Gln Glu His Leu Glu
                80             85             90

aaa acc aag ccg cac tgc gcg att tat tca ggg att tca aac caa tat      821
Lys Thr Lys Pro His Cys Ala Ile Tyr Ser Gly Ile Ser Asn Gln Tyr
                95             100             105

tta gac ggc atg gcc aaa ggg gcg aac cgt cgt ctt atc aag ctc ttt      869
Leu Asp Gly Met Ala Lys Gly Ala Asn Arg Arg Leu Ile Lys Leu Phe
                110             115             120

gaa aga gac gat att gcg att tac aac tcg ata cct aca gtc gaa ggt      917
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Glu Arg Asp Asp Ile Ala Ile Tyr Asn Ser Ile Pro Thr Val Glu Gly	
125 130 135	
gcc att atg atg gcc ata cag cat aca gac ttt acg att cac ggc tcg	965
Ala Ile Met Met Ala Ile Gln His Thr Asp Phe Thr Ile His Gly Ser	
140 145 150 155	
aat gta atg gtt ctc ggg ctg ggg cgg acg gga atg agc atc agc cgg	1013
Asn Val Met Val Leu Gly Leu Gly Arg Thr Gly Met Ser Ile Ser Arg	
160 165 170	
acg ttc tcg gcg ctc ggc gca cgc gta aaa gtc gga gct cgc gac tcc	1061
Thr Phe Ser Ala Leu Gly Ala Arg Val Lys Val Gly Ala Arg Asp Ser	
175 180 185	
gcc cac ctc gcc aga atc atg gag atg ggc ctc act cct ttc cac aca	1109
Ala His Leu Ala Arg Ile Met Glu Met Gly Leu Thr Pro Phe His Thr	
190 195 200	
aac gaa ctt gca gag cat gtt gaa aat atc gac ata tgc atc aat acc	1157
Asn Glu Leu Ala Glu His Val Glu Asn Ile Asp Ile Cys Ile Asn Thr	
205 210 215	
att cca agc ctg att ctc gat aaa cat gtc ctc tca cga atg aca ccc	1205
Ile Pro Ser Leu Ile Leu Asp Lys His Val Leu Ser Arg Met Thr Pro	
220 225 230 235	
aga aca tta att ctc gat tta gca acc cgt ccc gga ggc aca gat ttt	1253
Arg Thr Leu Ile Leu Asp Leu Ala Thr Arg Pro Gly Gly Thr Asp Phe	
240 245 250	
gat ttt gcc gaa aag caa ggc att aaa gcg ctg ctt gct cca gga ctt	1301
Asp Phe Ala Glu Lys Gln Gly Ile Lys Ala Leu Leu Ala Pro Gly Leu	
255 260 265	
ccc ggg atc gtc gcg cct aaa acg gcg gga cag atc att gcc aat gtt	1349
Pro Gly Ile Val Ala Pro Lys Thr Ala Gly Gln Ile Ile Ala Asn Val	
270 275 280	
ttg tgc aac ctt ttg tct gaa tta aca act gac cga aag ggg ctg tca	1397
Leu Cys Asn Leu Leu Ser Glu Leu Thr Thr Asp Arg Lys Gly Leu Ser	
285 290 295	
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atgccgtttt tccgcagatt gaagcgctga tcaacaaagg ggctgaagtc agaccggtcg	1517
tgacgcatac tgtcaagtcg acggatacac gctttggaga aggggaagaa tgggtcagaa	1577
gaatagaaga gctgactgga tttgaagtca ttgattccat tccgaaagct gagcctctcg	1637
ggccgaaaac accgctggac tgcattggtt ttgcgccatt gacgggaaat tcgatgagca	1697
agcttgcaaa cgcccagacg gacagtccgg ttctcatggc ggccaaagcg acgatgagaa	1757
actcccgtcc cgtcgtcctc ggcatttcaa cgaatgacgc gctcggcttg aacggcgctca	1817

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cttac 1882

<210> 93  
<211> 299  
<212> PRT  
<213> Bacillus licheniformis

<400> 93

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Ile Gly Phe Asp Gln Leu Asp His Gly Phe Thr Gly Ala Thr Lys Leu  
35 40 45

Lys Leu Asn Glu Leu Asp Phe Gly Thr Ile Asp Ser Ile Ile Leu Pro  
50 55 60

Val Ser Gly Thr Ser Met Glu Gly Thr Val Ala Thr Val Phe Ser Asn  
65 70 75 80

Glu Lys Val Val Leu Lys Gln Glu His Leu Glu Lys Thr Lys Pro His  
85 90 95

Cys Ala Ile Tyr Ser Gly Ile Ser Asn Gln Tyr Leu Asp Gly Met Ala  
100 105 110

Lys Gly Ala Asn Arg Arg Leu Ile Lys Leu Phe Glu Arg Asp Asp Ile  
115 120 125

Ala Ile Tyr Asn Ser Ile Pro Thr Val Glu Gly Ala Ile Met Met Ala  
130 135 140

Ile Gln His Thr Asp Phe Thr Ile His Gly Ser Asn Val Met Val Leu  
145 150 155 160

Gly Leu Gly Arg Thr Gly Met Ser Ile Ser Arg Thr Phe Ser Ala Leu  
165 170 175

Gly Ala Arg Val Lys Val Gly Ala Arg Asp Ser Ala His Leu Ala Arg



180	185	190
Ile Met Glu Met Gly Leu Thr Pro Phe His Thr Asn Glu Leu Ala Glu		
195	200	205
His Val Glu Asn Ile Asp Ile Cys Ile Asn Thr Ile Pro Ser Leu Ile		
210	215	220
Leu Asp Lys His Val Leu Ser Arg Met Thr Pro Arg Thr Leu Ile Leu		
225	230	235
Asp Leu Ala Thr Arg Pro Gly Gly Thr Asp Phe Asp Phe Ala Glu Lys		
245	250	255
Gln Gly Ile Lys Ala Leu Leu Ala Pro Gly Leu Pro Gly Ile Val Ala		
260	265	270
Pro Lys Thr Ala Gly Gln Ile Ile Ala Asn Val Leu Cys Asn Leu Leu		
275	280	285
Ser Glu Leu Thr Thr Asp Arg Lys Gly Leu Ser		
290	295	

<210> 94  
 <211> 1588  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1088)

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tcggcgctcg gcgcacgcgt aaaagtcgga gctcgcgact ccgcccacct cgccagaatc	180
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gacatatgca tcaataccat tccaagcctg attctcgata aacatgtcct ctcacgaatg	300
acaccagaa cattaattct cgatttagca acccgtcccg gaggcacaga ttttgatttt	360
gccgaaaagc aaggcattaa agcgtgctt gctccaggac ttcccgggat cgtcgcgcct	420
aaaacggcgg gacagatcat tgccaatgtt ttgtgcaacc ttttgtctga attaacaact	480

gaccgaaagg ggctgtcata atg tcg atc aaa gga aaa aga atc gga ttt ggc	533
Met Ser Ile Lys Gly Lys Arg Ile Gly Phe Gly	
1 5 10	
cta acg ggt tca cat tgt acg tat gat gcc gtt ttt ccg cag att gaa	581
Leu Thr Gly Ser His Cys Thr Tyr Asp Ala Val Phe Pro Gln Ile Glu	
15 20 25	
gcg ctg atc aac aaa ggg gct gaa gtc aga ccg gtc gtg acg cat act	629
Ala Leu Ile Asn Lys Gly Ala Glu Val Arg Pro Val Val Thr His Thr	
30 35 40	
gtc aag tcg acg gat aca cgc ttt gga gaa ggg gaa gaa tgg gtc aga	677
Val Lys Ser Thr Asp Thr Arg Phe Gly Glu Gly Glu Glu Trp Val Arg	
45 50 55	
aga ata gaa gag ctg act gga ttt gaa gtc att gat tcc att ccg aaa	725
Arg Ile Glu Glu Leu Thr Gly Phe Glu Val Ile Asp Ser Ile Pro Lys	
60 65 70 75	
gct gag cct ctc ggg ccg aaa aca ccg ctg gac tgc atg gtt gtt gcg	773
Ala Glu Pro Leu Gly Pro Lys Thr Pro Leu Asp Cys Met Val Val Ala	
80 85 90	
cca ttg acg gga aat tcg atg agc aag ctt gca aac gcc cag acg gac	821
Pro Leu Thr Gly Asn Ser Met Ser Lys Leu Ala Asn Ala Gln Thr Asp	
95 100 105	
agt ccg gtt ctc atg gcg gcc aaa gcg acg atg aga aac tcc cgt ccc	869
Ser Pro Val Leu Met Ala Ala Lys Ala Thr Met Arg Asn Ser Arg Pro	
110 115 120	
gtc gtc ctc ggc att tca acg aat gac gcg ctc ggc ttg aac ggc gtc	917
Val Val Leu Gly Ile Ser Thr Asn Asp Ala Leu Gly Leu Asn Gly Val	
125 130 135	
aac ttg atg agg ctg atg gcg gca aaa aat gtt tac ttt att ccg ttc	965
Asn Leu Met Arg Leu Met Ala Ala Lys Asn Val Tyr Phe Ile Pro Phe	
140 145 150 155	
ggc cag gat gac cct tac aaa aag ccg aat tcg ctc gtc gcc aaa atg	1013
Gly Gln Asp Asp Pro Tyr Lys Lys Pro Asn Ser Leu Val Ala Lys Met	
160 165 170	
gat ctt tta gtg ccg gcg gtc gaa gaa gcg ctc tcc cat aaa caa ata	1061
Asp Leu Leu Val Pro Ala Val Glu Glu Ala Leu Ser His Lys Gln Ile	
175 180 185	
cag cct atc ctg gtc cat aat gat caa taaatctttt gaaaataaag	1108
Gln Pro Ile Leu Val His Asn Asp Gln	
190 195	
atgtaacaaa aaatatcaat caccacggca cacatctatg ttaaaataaa atgtaaaatg	1168
catagtcaac caatcgttta cgacgattaa ggtggaagga gttttacaat tgggcagagg	1228

attacatgta gcagtagttg gtgcgacagg cgctgtagga cagcaaagt taaaaacact 1288  
agaagacagg aattttgaac tggataaact gactttatta tcctcaaaac gttcagcagg 1348  
tacgaaactg actttcaaag gcgaagagta cacagtagaa gaagctcgtc ctgagagctt 1408  
tgaaggcgtc aacatcgcg c ttttcagcgc cgggggaagc gtttcgcagg cgcttgctca 1468  
cgaggctgtc aaacgcgggg cgatcgatcat tgataatacg agcgcgttcc ggatggacca 1528  
aaacactccg ctcgctgtac ctgaggtcaa tgaggaagat ttgcacaagc acaacgggat 1588

<210> 95  
<211> 196  
<212> PRT  
<213> Bacillus licheniformis

<400> 95

Met Ser Ile Lys Gly Lys Arg Ile Gly Phe Gly Leu Thr Gly Ser His  
1 5 10 15

Cys Thr Tyr Asp Ala Val Phe Pro Gln Ile Glu Ala Leu Ile Asn Lys  
20 25 30

Gly Ala Glu Val Arg Pro Val Val Thr His Thr Val Lys Ser Thr Asp  
35 40 45

Thr Arg Phe Gly Glu Gly Glu Glu Trp Val Arg Arg Ile Glu Glu Leu  
50 55 60

Thr Gly Phe Glu Val Ile Asp Ser Ile Pro Lys Ala Glu Pro Leu Gly  
65 70 75 80

Pro Lys Thr Pro Leu Asp Cys Met Val Val Ala Pro Leu Thr Gly Asn  
85 90 95

Ser Met Ser Lys Leu Ala Asn Ala Gln Thr Asp Ser Pro Val Leu Met  
100 105 110

Ala Ala Lys Ala Thr Met Arg Asn Ser Arg Pro Val Val Leu Gly Ile  
115 120 125

Ser Thr Asn Asp Ala Leu Gly Leu Asn Gly Val Asn Leu Met Arg Leu  
130 135 140

Met Ala Ala Lys Asn Val Tyr Phe Ile Pro Phe Gly Gln Asp Asp Pro

[illegible]

caa acc cgg gag tat gca gag ctg cct gcg aca agc cga ttt gta gaa	725
Gln Thr Arg Glu Tyr Ala Glu Leu Pro Ala Thr Ser Arg Phe Val Glu	
60 65 70 75	
gat gta aag ctg aaa ggg gac ggc agc gca gag ctg acg cat tgt ttc	773
Asp Val Lys Leu Lys Gly Asp Gly Ser Ala Glu Leu Thr His Cys Phe	
80 85 90	
cca gtg gat atc acc atc ccg aaa gac aaa gtc aat cat tta aac gac	821
Pro Val Asp Ile Thr Ile Pro Lys Asp Lys Val Asn His Leu Asn Asp	
95 100 105	
gta ttt gtt ttt att gac gct ttc gat tat cag ctg aca gat gcg agg	869
Val Phe Val Phe Ile Asp Ala Phe Asp Tyr Gln Leu Thr Asp Ala Arg	
110 115 120	
atg ctg acg att cag gct gat ttg gcg att gaa ggc ctc ttg aat gtg	917
Met Leu Thr Ile Gln Ala Asp Leu Ala Ile Glu Gly Leu Leu Asn Val	
125 130 135	
agc ggt gaa gcg ggt gaa gaa gaa ccg cgc act atg cct gcg gcc gtc	965
Ser Gly Glu Ala Gly Glu Glu Glu Pro Arg Thr Met Pro Ala Ala Val	
140 145 150 155	
cat ccg gaa gag gag ctc gaa cct gcc tac aga tca cct tca aac gac	1013
His Pro Glu Glu Glu Leu Glu Pro Ala Tyr Arg Ser Pro Ser Asn Asp	
160 165 170	
gaa gat cag ggt gaa gag aaa gaa tat ttg atc cag ctt gac aga cct	1061
Glu Asp Gln Gly Glu Glu Lys Glu Tyr Leu Ile Gln Leu Asp Arg Pro	
175 180 185	
tac gaa gag cag gac gaa gaa cag gcg gaa gaa cat gat acc ggt gag	1109
Tyr Glu Glu Gln Asp Glu Glu Gln Ala Glu Glu His Asp Thr Gly Glu	
190 195 200	
gaa acg gtt ccg att tac cag tcg ttt ctc gga aac gac aca gag gaa	1157
Glu Thr Val Pro Ile Tyr Gln Ser Phe Leu Gly Asn Asp Thr Glu Glu	
205 210 215	
gct aaa ccg ttt ttt aca gcg tct ttg tcg gcg gca gag cgt acg aag	1205
Ala Lys Pro Phe Phe Thr Ala Ser Leu Ser Ala Ala Glu Arg Thr Lys	
220 225 230 235	
cgc gaa ata gaa aat caa aaa gaa gcc tct ctt gaa cag ccg gaa gaa	1253
Arg Glu Ile Glu Asn Gln Lys Glu Ala Ser Leu Glu Gln Pro Glu Glu	
240 245 250	
gaa tat aag ctg aaa aga gag aaa gtg gaa gag gaa ccg gaa gaa tat	1301
Glu Tyr Lys Leu Lys Arg Glu Lys Val Glu Glu Glu Pro Glu Glu Tyr	
255 260 265	
gag ctg aaa aga gag aaa gtg gaa gag gaa ccg gaa gaa tat gag ctg	1349
Glu Leu Lys Arg Glu Lys Val Glu Glu Glu Pro Glu Glu Tyr Glu Leu	
270 275 280	

aaa aga gaa gaa gcg gaa gaa gag ccg gag ctg tcg cac agc tct tat	1397
Lys Arg Glu Glu Ala Glu Glu Glu Pro Glu Leu Ser His Ser Ser Tyr	
285 290 295	
caa cct cac gag gaa ctg aaa gag aac ccg ttc tac agt gtt cct cct	1445
Gln Pro His Glu Glu Leu Lys Glu Asn Pro Phe Tyr Ser Val Pro Pro	
300 305 310 315	
ctt ctg aag gaa gac cag aat gac agg gag cct gag gct ttt gag gtt	1493
Leu Leu Lys Glu Asp Gln Asn Asp Arg Glu Pro Glu Ala Phe Glu Val	
320 325 330	
gag gtg aca cag gaa gca gaa gcg att gat gaa gaa gag gaa gcc ggg	1541
Glu Val Thr Gln Glu Ala Glu Ala Ile Asp Glu Glu Glu Glu Ala Gly	
335 340 345	
cat acg att gaa atc ccg gaa tat tcg ttt cat gag cag acg gag ccc	1589
His Thr Ile Glu Ile Pro Glu Tyr Ser Phe His Glu Gln Thr Glu Pro	
350 355 360	
gaa gaa gaa aga gat gaa atg cag gca gcg gat gaa cag gaa gtg tca	1637
Glu Glu Glu Arg Asp Glu Met Gln Ala Ala Asp Glu Gln Glu Val Ser	
365 370 375	
gca aag gaa aac gac aac gca ctc tat ttg aca aag ctg ttt aca aag	1685
Ala Lys Glu Asn Asp Asn Ala Leu Tyr Leu Thr Lys Leu Phe Thr Lys	
380 385 390 395	
cag gga gag gag gag ttt act cga atg agg atg tgc atc gtt cag caa	1733
Gln Gly Glu Glu Glu Phe Thr Arg Met Arg Met Cys Ile Val Gln Gln	
400 405 410	
aat gat acg att gat ctt ctg tgc gag cgc tat gat att aac gtc cag	1781
Asn Asp Thr Ile Asp Leu Leu Cys Glu Arg Tyr Asp Ile Asn Val Gln	
415 420 425	
cag ctc atc cgg atg aat tcc ctt tcc ctt gac gag gaa tta aaa gag	1829
Gln Leu Ile Arg Met Asn Ser Leu Ser Leu Asp Glu Glu Leu Lys Glu	
430 435 440	
gga cag atc ctt tat ata ccg gat tat caa aac agc cat gcc	1871
Gly Gln Ile Leu Tyr Ile Pro Asp Tyr Gln Asn Ser His Ala	
445 450 455	
taatgcattg ataaaaatgt ggtgaagccg atggaaggca tccagtctgt tttaaatgag	1931
tacggtctta cgctgaata tatggagtcc gtcagttcaa aggtgtggaa agtgtatacg	1991
gatcacggtg tatttgctct gaaaaaattg gcggcttcaa gaaacacccg cttcacggaa	2051
cagatgatca tgctggagga aaaaggctac aggagttcg ttctgtcta tcgaaaccgc	2111
acaggcgaat ttttaacgca agccggagaa gatgtctgct atctcatgcc ctggct	2167

<210> 97  
<211> 457

<212> PRT

<213> Bacillus licheniformis

<400> 97

Leu Pro Gln Asn Asn Arg Leu Gln Phe Ser Val Glu Glu Ser Ile Cys  
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Phe Gln Lys Gly Gln Glu Val Ser Glu Leu Leu Ser Ile Ser Leu Asp  
20 25 30

Pro Asp Ile Thr Val Gln Glu Val Asn Asp Tyr Val Ser Ile Arg Gly  
35 40 45

Ser Leu Glu Leu Thr Gly Glu Tyr Asn Ile Asp Gln Thr Arg Glu Tyr  
50 55 60

Ala Glu Leu Pro Ala Thr Ser Arg Phe Val Glu Asp Val Lys Leu Lys  
65 70 75 80

Gly Asp Gly Ser Ala Glu Leu Thr His Cys Phe Pro Val Asp Ile Thr  
85 90 95

Ile Pro Lys Asp Lys Val Asn His Leu Asn Asp Val Phe Val Phe Ile  
100 105 110

Asp Ala Phe Asp Tyr Gln Leu Thr Asp Ala Arg Met Leu Thr Ile Gln  
115 120 125

Ala Asp Leu Ala Ile Glu Gly Leu Leu Asn Val Ser Gly Glu Ala Gly  
130 135 140

Glu Glu Glu Pro Arg Thr Met Pro Ala Ala Val His Pro Glu Glu Glu  
145 150 155 160

Leu Glu Pro Ala Tyr Arg Ser Pro Ser Asn Asp Glu Asp Gln Gly Glu  
165 170 175

Glu Lys Glu Tyr Leu Ile Gln Leu Asp Arg Pro Tyr Glu Glu Gln Asp  
180 185 190

Glu Glu Gln Ala Glu Glu His Asp Thr Gly Glu Glu Thr Val Pro Ile  
195 200 205

Tyr Gln Ser Phe Leu Gly Asn Asp Thr Glu Glu Ala Lys Pro Phe Phe  
 210 215 220

Thr Ala Ser Leu Ser Ala Ala Glu Arg Thr Lys Arg Glu Ile Glu Asn  
 225 230 235 240

Gln Lys Glu Ala Ser Leu Glu Gln Pro Glu Glu Glu Tyr Lys Leu Lys  
 245 250 255

Arg Glu Lys Val Glu Glu Glu Pro Glu Glu Tyr Glu Leu Lys Arg Glu  
 260 265 270

Lys Val Glu Glu Glu Pro Glu Glu Tyr Glu Leu Lys Arg Glu Glu Ala  
 275 280 285

Glu Glu Glu Pro Glu Leu Ser His Ser Ser Tyr Gln Pro His Glu Glu  
 290 295 300

Leu Lys Glu Asn Pro Phe Tyr Ser Val Pro Pro Leu Leu Lys Glu Asp  
 305 310 315 320

Gln Asn Asp Arg Glu Pro Glu Ala Phe Glu Val Glu Val Thr Gln Glu  
 325 330 335

Ala Glu Ala Ile Asp Glu Glu Glu Glu Ala Gly His Thr Ile Glu Ile  
 340 345 350

Pro Glu Tyr Ser Phe His Glu Gln Thr Glu Pro Glu Glu Glu Arg Asp  
 355 360 365

Glu Met Gln Ala Ala Asp Glu Gln Glu Val Ser Ala Lys Glu Asn Asp  
 370 375 380

Asn Ala Leu Tyr Leu Thr Lys Leu Phe Thr Lys Gln Gly Glu Glu Glu  
 385 390 395 400

Phe Thr Arg Met Arg Met Cys Ile Val Gln Gln Asn Asp Thr Ile Asp  
 405 410 415

Leu Leu Cys Glu Arg Tyr Asp Ile Asn Val Gln Gln Leu Ile Arg Met  
 420 425 430

Asn Ser Leu Ser Leu Asp Glu Glu Leu Lys Glu Gly Gln Ile Leu Tyr



435

440

445

Ile Pro Asp Tyr Gln Asn Ser His Ala  
450 455

<210> 98  
<211> 1955  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(1463)

<400> 98  
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tcaaagctta ttattacgaa agataactat attatgttca gtaacagaat catgaagaca 120  
aaaaaggcga atttcatttc cttcaaatca aaaagacttt ggtgaagatc ccgctgtgaa 180  
acaggggaga gccgagcagc gcctgcagca catcttcaga cagattgggt ccattccccg 240  
aaggacctca tcaatcacca ctttctcccg atttgccatg tcaacctgtt aagcatttac 300  
caaacaggat gaaaaaattg gtttgtccgc acagcttacc tgaatacaat aaaaaataaa 360  
gtattttctcg ggaaagcgca ggtttcaaca agacctgccc cgttcttgtc aaaaagcatt 420  
ggattgtgca gtcattgtggg cgtctgtcac ggcataagcg cgccatgaat aggatataaa 480  
gagagaatgg tgagggtgagt gtg ttg gaa agg gct gtt act tat aaa aac aac 533  
Val Leu Glu Arg Ala Val Thr Tyr Lys Asn Asn  
1 5 10  
gga caa atc aat atc ata ttg aac ggt caa aag cag gtt ttg gcc aat 581  
Gly Gln Ile Asn Ile Ile Leu Asn Gly Gln Lys Gln Val Leu Ala Asn  
15 20 25  
tca gag gct gaa gcc gaa tat cag gcc gca ctg caa aaa aat gaa gcc 629  
Ser Glu Ala Glu Ala Glu Tyr Gln Ala Ala Leu Gln Lys Asn Glu Ala  
30 35 40  
aaa cac agc att ctg aaa gaa att gaa agg gaa atg aac acg ctg gtc 677  
Lys His Ser Ile Leu Lys Glu Ile Glu Arg Glu Met Asn Thr Leu Val  
45 50 55  
gga atg gag gaa atg aag cgc aat atc aag gaa atc tac gcc tgg att 725  
Gly Met Glu Glu Met Lys Arg Asn Ile Lys Glu Ile Tyr Ala Trp Ile  
60 65 70 75  
ttc gtt aat aaa aag cgc gaa gaa caa ggc ctt aag gcc gga aaa cag 773  
Phe Val Asn Lys Lys Arg Glu Glu Gln Gly Leu Lys Ala Gly Lys Gln  
80 85 90

gcg ctt cac atg atg ttc aaa gga aat ccg gga acc gga aaa acg acc	821
Ala Leu His Met Met Phe Lys Gly Asn Pro Gly Thr Gly Lys Thr Thr	
95 100 105	
gtc gcc agg ctg atc ggc agg ctt ttt tac gaa atg aat gtt ctc tca	869
Val Ala Arg Leu Ile Gly Arg Leu Phe Tyr Glu Met Asn Val Leu Ser	
110 115 120	
aaa ggc cat ctg atc gag gcg gag cgc gcc gat ctc gtc ggt gag tac	917
Lys Gly His Leu Ile Glu Ala Glu Arg Ala Asp Leu Val Gly Glu Tyr	
125 130 135	
atc ggc cat acg gcg caa aaa acg agg gat tta atc aaa aaa gcg atg	965
Ile Gly His Thr Ala Gln Lys Thr Arg Asp Leu Ile Lys Lys Ala Met	
140 145 150 155	
ggc gga atc ctg ttc atc gat gaa gcc tat tcc ctt gcc aga ggc gga	1013
Gly Gly Ile Leu Phe Ile Asp Glu Ala Tyr Ser Leu Ala Arg Gly Gly	
160 165 170	
gag aaa gac ttc ggc aag gag gca atc gat aca ttg gtc aaa cat atg	1061
Glu Lys Asp Phe Gly Lys Glu Ala Ile Asp Thr Leu Val Lys His Met	
175 180 185	
gag gat aag cgc aac gaa ttc att tta atc ctc gcc gga tat tcg cgg	1109
Glu Asp Lys Arg Asn Glu Phe Ile Leu Ile Leu Ala Gly Tyr Ser Arg	
190 195 200	
gaa atg gat cat ttt ctt tca tta aac ccg ggc ctt cag tca agg ttt	1157
Glu Met Asp His Phe Leu Ser Leu Asn Pro Gly Leu Gln Ser Arg Phe	
205 210 215	
ccg atc agc atc gat ttt ccc gat tac tca gtc agc cag ctg atg gac	1205
Pro Ile Ser Ile Asp Phe Pro Asp Tyr Ser Val Ser Gln Leu Met Asp	
220 225 230 235	
att gca aaa cgg atg atg gcg gaa agg gaa tat cag ttc agc cct gag	1253
Ile Ala Lys Arg Met Met Ala Glu Arg Glu Tyr Gln Phe Ser Pro Glu	
240 245 250	
gct gaa tgg aag ctg aaa gac cat ctg atg gcc gtc aaa agt acg gtc	1301
Ala Glu Trp Lys Leu Lys Asp His Leu Met Ala Val Lys Ser Thr Val	
255 260 265	
agc ccc gcg aag ttc agc aat ggc cgt ttc gtc cgc aac ctg atc gaa	1349
Ser Pro Ala Lys Phe Ser Asn Gly Arg Phe Val Arg Asn Leu Ile Glu	
270 275 280	
aaa tcc atc cgg tcg cag gcg atg aga ctg ctg atg gga gac tgc tac	1397
Lys Ser Ile Arg Ser Gln Ala Met Arg Leu Leu Met Gly Asp Cys Tyr	
285 290 295	
tta aag aat gac ttg ata acc atc aaa agc cag gat ctc gac ttg aag	1445
Leu Lys Asn Asp Leu Ile Thr Ile Lys Ser Gln Asp Leu Asp Leu Lys	
300 305 310 315	

gaa gac gcg ccg cac gta taatggcgcg ttcttttttt attttcgagg 1493  
 Glu Asp Ala Pro His Val  
 320

atttctggca accgctccct tcgtttgtta tgatagtact gcttattgac taacgttaag 1553  
 aaaggaacat gatcacttga acgaacagga agtcatgaaa gagaaagcca tattagtcgg 1613  
 atgccagctt cgcacgtgt ctgatgagcg tttttcatac tcgatggaag agctcgccgc 1673  
 gctgacgaaa acggccgacg gaacggttgt ttccacggtc acgcagaagc ggaaccgtgt 1733  
 ggatgctgct acatatatcg gaaaaggaaa agtagatgaa ttggcggtgc tctgtgaaga 1793  
 gctgtcgccc gatgttttaa tttttaatga tgaattgtcg ccgagtcagc tgaaagcgct 1853  
 tgtcacaacg cttgacgtga aaatcatcga ccggacgcag ttgatccttg atattttcgc 1913  
 caaacgcgcg aggacaaggg aaggaaagct gcaaattgag ct 1955

<210> 99  
 <211> 321  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 99

Val Leu Glu Arg Ala Val Thr Tyr Lys Asn Asn Gly Gln Ile Asn Ile  
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Ile Leu Asn Gly Gln Lys Gln Val Leu Ala Asn Ser Glu Ala Glu Ala  
 20 25 30

Glu Tyr Gln Ala Ala Leu Gln Lys Asn Glu Ala Lys His Ser Ile Leu  
 35 40 45

Lys Glu Ile Glu Arg Glu Met Asn Thr Leu Val Gly Met Glu Glu Met  
 50 55 60

Lys Arg Asn Ile Lys Glu Ile Tyr Ala Trp Ile Phe Val Asn Lys Lys  
 65 70 75 80

Arg Glu Glu Gln Gly Leu Lys Ala Gly Lys Gln Ala Leu His Met Met  
 85 90 95

Phe Lys Gly Asn Pro Gly Thr Gly Lys Thr Thr Val Ala Arg Leu Ile  
 100 105 110

Gly Arg Leu Phe Tyr Glu Met Asn Val Leu Ser Lys Gly His Leu Ile

115	120	125
Glu Ala Glu Arg Ala Asp Leu Val Gly Glu Tyr Ile Gly His Thr Ala		
130	135	140
Gln Lys Thr Arg Asp Leu Ile Lys Lys Ala Met Gly Gly Ile Leu Phe		
145	150	155
Ile Asp Glu Ala Tyr Ser Leu Ala Arg Gly Gly Glu Lys Asp Phe Gly		
165	170	175
Lys Glu Ala Ile Asp Thr Leu Val Lys His Met Glu Asp Lys Arg Asn		
180	185	190
Glu Phe Ile Leu Ile Leu Ala Gly Tyr Ser Arg Glu Met Asp His Phe		
195	200	205
Leu Ser Leu Asn Pro Gly Leu Gln Ser Arg Phe Pro Ile Ser Ile Asp		
210	215	220
Phe Pro Asp Tyr Ser Val Ser Gln Leu Met Asp Ile Ala Lys Arg Met		
225	230	235
Met Ala Glu Arg Glu Tyr Gln Phe Ser Pro Glu Ala Glu Trp Lys Leu		
245	250	255
Lys Asp His Leu Met Ala Val Lys Ser Thr Val Ser Pro Ala Lys Phe		
260	265	270
Ser Asn Gly Arg Phe Val Arg Asn Leu Ile Glu Lys Ser Ile Arg Ser		
275	280	285
Gln Ala Met Arg Leu Leu Met Gly Asp Cys Tyr Leu Lys Asn Asp Leu		
290	295	300
Ile Thr Ile Lys Ser Gln Asp Leu Asp Leu Lys Glu Asp Ala Pro His		
305	310	315
		320
Val		

<210> 100  
 <211> 2082

<212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1607)

<400> 100  
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 gaattttcta aaacgcctcg tgccgaaaca tgctcaagaa tcggctataa ctttcagcgg 120  
 aggcggaat acaaggccgc tatctactgg tatgagctgg ccacaacatt ggtgcctgat 180  
 tcaaataaat ggagcttcac ctatccggca tactatactt ggtaccctca ttgcaaattg 240  
 tgtgtgtgct attacaattt aggagacttt gaaaagtcgt atcatcataa tgaagaggcg 300  
 aggaaatacc gtcccgaaga caaatccgtc cttcataaca aacagctgct ggaagggaaa 360  
 ttaggcatta acaattagca ttgtaaagac ttactgaaca agtaggtctt ttttttatga 420  
 ataaaatcaa gccgtgccaa tttagcggca ggcatcataa cttatttttg aactttttga 480  
 atttagagga ggaacaaagg atg atc ccg tta gtc aat tta aaa cgt caa ttt 533  
                                   Met Ile Pro Leu Val Asn Leu Lys Arg Gln Phe  
                                   1                                  5                                  10  
 caa aca gta aaa cag gat att tta aaa gag ttt gaa cat gtg ctg gac 581  
 Gln Thr Val Lys Gln Asp Ile Leu Lys Glu Phe Glu His Val Leu Asp  
                                   15                                  20                                  25  
 agc ggc caa tat ata ttg ggg cca aag gtt gaa gaa tta gag aaa aga 629  
 Ser Gly Gln Tyr Ile Leu Gly Pro Lys Val Glu Glu Leu Glu Lys Arg  
                                   30                                  35                                  40  
 ata gct gaa aag ctt ggt gta aaa gaa gcg gtc gcg gtc gcc aac gga 677  
 Ile Ala Glu Lys Leu Gly Val Lys Glu Ala Val Ala Val Ala Asn Gly  
                                   45                                  50                                  55  
 acg gat gca ttg gtg ctg acg ctt gaa gct ttc ggc atc ggc aaa ggg 725  
 Thr Asp Ala Leu Val Leu Thr Leu Glu Ala Phe Gly Ile Gly Lys Gly  
                                   60                                  65                                  70                                  75  
 gat gaa gtg att acg acc ccg ttc act ttt ttc gcc acc gcc gaa gcc 773  
 Asp Glu Val Ile Thr Thr Pro Phe Thr Phe Phe Ala Thr Ala Glu Ala  
                                   80                                  85                                  90  
 gtc tca agg gtg ggg gct gaa cct gtg ttt gct gat gtc gat cct gaa 821  
 Val Ser Arg Val Gly Ala Glu Pro Val Phe Ala Asp Val Asp Pro Glu  
                                   95                                  100                                  105  
 aca tac aat ctt gat ccg aaa aaa ata gaa gaa aag atc acc cct gct 869  
 Thr Tyr Asn Leu Asp Pro Lys Lys Ile Glu Glu Lys Ile Thr Pro Ala  
                                   110                                  115                                  120

act aaa gcg atc att ccc gtc cat atc ttc gga cag ccg gct gat atg	917
Thr Lys Ala Ile Ile Pro Val His Ile Phe Gly Gln Pro Ala Asp Met	
125 130 135	
gac gag atc atg gag ctt gcc aaa aaa cac gga ctg ctt gtg att gag	965
Asp Glu Ile Met Glu Leu Ala Lys Lys His Gly Leu Leu Val Ile Glu	
140 145 150 155	
gat gcc tgc caa gcg ttc ggc gca tcg tat aaa gag cgg cct gtc ggc	1013
Asp Ala Cys Gln Ala Phe Gly Ala Ser Tyr Lys Glu Arg Pro Val Gly	
160 165 170	
agc atc ggg gat gcc gcc tgt ttt tca ttt ttc cct aca aaa aac ttg	1061
Ser Ile Gly Asp Ala Ala Cys Phe Ser Phe Phe Pro Thr Lys Asn Leu	
175 180 185	
gga aca ttg gga gac ggg gga atg gtg acg att tca gac ccg gat gca	1109
Gly Thr Leu Gly Asp Gly Gly Met Val Thr Ile Ser Asp Pro Asp Ala	
190 195 200	
gcc cgg caa tta aga aca ctc aga acc cat ggc act agc aaa aaa tac	1157
Ala Arg Gln Leu Arg Thr Leu Arg Thr His Gly Thr Ser Lys Lys Tyr	
205 210 215	
ttc cat gac aaa atc ggt ttc aac agc cgt ctt gat gaa tta cac gcc	1205
Phe His Asp Lys Ile Gly Phe Asn Ser Arg Leu Asp Glu Leu His Ala	
220 225 230 235	
gca gct tta ctc att ctt ctt gag aaa atc gac ggc tgg aat gaa caa	1253
Ala Ala Leu Leu Ile Leu Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln	
240 245 250	
aga aga aga gtg gcc agc cgc tac aga gaa ggt ttg aaa acg gcg gag	1301
Arg Arg Arg Val Ala Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu	
255 260 265	
cac ctc aca ctg ccg gca gag aaa gag gac cgc aca cat atc tat cat	1349
His Leu Thr Leu Pro Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His	
270 275 280	
ctc tat tgt atc ggc gcg aaa aac cgc gac tac atc ata caa tcg ctg	1397
Leu Tyr Cys Ile Gly Ala Lys Asn Arg Asp Tyr Ile Ile Gln Ser Leu	
285 290 295	
aaa gag cag gac att cat tca ggt gtg tat tat cct tgc tgc ctt cat	1445
Lys Glu Gln Asp Ile His Ser Gly Val Tyr Tyr Pro Cys Cys Leu His	
300 305 310 315	
ctg caa tcg gtc tat tct tca ctg cag tac aaa aaa ggc gat ttt cct	1493
Leu Gln Ser Val Tyr Ser Ser Leu Gln Tyr Lys Lys Gly Asp Phe Pro	
320 325 330	
ata gcc gag tcc ttg tcc gaa acc ctt ttc gcc att ccg atg gat cct	1541
Ile Ala Glu Ser Leu Ser Glu Thr Leu Phe Ala Ile Pro Met Asp Pro	
335 340 345	
ttt cta gcc gcc gag gaa caa gat cag att att tct gcg ctg ctg aaa	1589

Phe Leu Ala Ala Glu Glu Gln Asp Gln Ile Ile Ser Ala Leu Leu Lys  
350 355 360

aaa gga gga ggg gaa aag tgacgggttca ttttggttta atcggctgcg 1637  
Lys Gly Gly Gly Glu Lys  
365

gctatatgtc aagaaaacat cttcaagcac tggccgagtg cgatgatgca aagttgtcgg 1697  
ccgtcagtgga tttgcaggaa gaaagaatga aggaagcggga agaatactat gcttcacctg 1757  
ccggtgagga aagccgaatg acccgctatc cgcagtatca agcgctgctt tcagatccta 1817  
aaattgaagc ggtcattatt gcggcggttt cgggactgca cgccgaaatg gccaaacatg 1877  
cgctgctggc aggcaagcac gtcacgtcg aaaaaccgat gaccttgtca ttacgggatg 1937  
ccgatgagct tatagaactg gcggagcaga acgggctgaa gctcatggtc tgccaccaga 1997  
tgcgccaccg gccgatcatg aaaaaactga aggaaacgat tgaggaagga aagctgggaa 2057  
agatctactt gggcacggta tcgct 2082

<210> 101  
<211> 369  
<212> PRT  
<213> Bacillus licheniformis

<400> 101

Met Ile Pro Leu Val Asn Leu Lys Arg Gln Phe Gln Thr Val Lys Gln  
1 5 10 15

Asp Ile Leu Lys Glu Phe Glu His Val Leu Asp Ser Gly Gln Tyr Ile  
20 25 30

Leu Gly Pro Lys Val Glu Glu Leu Glu Lys Arg Ile Ala Glu Lys Leu  
35 40 45

Gly Val Lys Glu Ala Val Ala Val Ala Asn Gly Thr Asp Ala Leu Val  
50 55 60

Leu Thr Leu Glu Ala Phe Gly Ile Gly Lys Gly Asp Glu Val Ile Thr  
65 70 75 80

Thr Pro Phe Thr Phe Phe Ala Thr Ala Glu Ala Val Ser Arg Val Gly  
85 90 95

Ala Glu Pro Val Phe Ala Asp Val Asp Pro Glu Thr Tyr Asn Leu Asp  
100 105 110

Pro Lys Lys Ile Glu Glu Lys Ile Thr Pro Ala Thr Lys Ala Ile Ile  
115 120 125

Pro Val His Ile Phe Gly Gln Pro Ala Asp Met Asp Glu Ile Met Glu  
130 135 140

Leu Ala Lys Lys His Gly Leu Leu Val Ile Glu Asp Ala Cys Gln Ala  
145 150 155 160

Phe Gly Ala Ser Tyr Lys Glu Arg Pro Val Gly Ser Ile Gly Asp Ala  
165 170 175

Ala Cys Phe Ser Phe Phe Pro Thr Lys Asn Leu Gly Thr Leu Gly Asp  
180 185 190

Gly Gly Met Val Thr Ile Ser Asp Pro Asp Ala Ala Arg Gln Leu Arg  
195 200 205

Thr Leu Arg Thr His Gly Thr Ser Lys Lys Tyr Phe His Asp Lys Ile  
210 215 220

Gly Phe Asn Ser Arg Leu Asp Glu Leu His Ala Ala Ala Leu Leu Ile  
225 230 235 240

Leu Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln Arg Arg Arg Val Ala  
245 250 255

Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu His Leu Thr Leu Pro  
260 265 270

Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His Leu Tyr Cys Ile Gly  
275 280 285

Ala Lys Asn Arg Asp Tyr Ile Ile Gln Ser Leu Lys Glu Gln Asp Ile  
290 295 300

His Ser Gly Val Tyr Tyr Pro Cys Cys Leu His Leu Gln Ser Val Tyr  
305 310 315 320

Ser Ser Leu Gln Tyr Lys Lys Gly Asp Phe Pro Ile Ala Glu Ser Leu  
325 330 335



Ser Glu Thr Leu Phe Ala Ile Pro Met Asp Pro Phe Leu Ala Ala Glu  
340 345 350

Glu Gln Asp Gln Ile Ile Ser Ala Leu Leu Lys Lys Gly Gly Gly Glu  
355 360 365

Lys

<210> 102  
<211> 1975  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(1472)

<400> 102  
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ccaaaaggct gatttgatca ttgatcagct tcatatcggc agctacggat tatttgccgt 180  
cgaatcgatg gcaatgggga aaccgcgttat ctgctggatc agtgatttta tgaaggatca 240  
ctatccttcc gaactgcctc ttataagagc aaatcccgcc aacattacag aggtgattga 300  
aaatgtgctt aaaaaccggg atatgctgcc ggaaatcggc cagaaaggaa gaaagtatgc 360  
agaagttcat catgatatgg tgaaaaacag caaaaaaaca ttggctgttt atcagtcgct 420  
actttcggaa tgaagttgaa caactttccc gtcgcgggat ttgtatgtaa aaaaaaacga 480  
aacaagcagg tgaacaattg atg agc gat atg aca gag tta tcc ggc cag cat 533  
Met Ser Asp Met Thr Glu Leu Ser Gly Gln His  
1 5 10  
att ttc ata act ggc gga gca ggc ttt atc gga tcc tct tta ata gga 581  
Ile Phe Ile Thr Gly Gly Ala Gly Phe Ile Gly Ser Ser Leu Ile Gly  
15 20 25  
aag ctg ata gag cgc aac agc gtc acc gta tat gac aat ttt tca aga 629  
Lys Leu Ile Glu Arg Asn Ser Val Thr Val Tyr Asp Asn Phe Ser Arg  
30 35 40  
gac tcc ctc cgg tat aag cct tac cgg gac cat cct cac ttg aaa gtg 677  
Asp Ser Leu Arg Tyr Lys Pro Tyr Arg Asp His Pro His Leu Lys Val  
45 50 55  
ctg cag gga gac att ttg gat ttg aac gcg ctt aaa aag gcg atc cag 725

Leu Gln Gly Asp Ile Leu Asp Leu Asn Ala Leu Lys Lys Ala Ile Gln	
60 65 70 75	
ggg gcc agc cac att gtc cac gcc gcc ggc atc gct ggg att gac acg	773
Gly Ala Ser His Ile Val His Ala Ala Gly Ile Ala Gly Ile Asp Thr	
80 85 90	
gtc att caa aac ccg gtt aaa acg atg cag gtc aac atg atc ggt tca	821
Val Ile Gln Asn Pro Val Lys Thr Met Gln Val Asn Met Ile Gly Ser	
95 100 105	
gcc aat ctg ctt gaa gcg gct gcc ggt tta acc gaa tgc aaa agg gtt	869
Ala Asn Leu Leu Glu Ala Ala Gly Leu Thr Glu Cys Lys Arg Val	
110 115 120	
gtc tgt ttc agt aca agc gaa gtg ttc ggc caa atc gct ttc aga gcg	917
Val Cys Phe Ser Thr Ser Glu Val Phe Gly Gln Ile Ala Phe Arg Ala	
125 130 135	
cgc gag acc agt cat act gtt tta gga gcg gtg gga gaa gcc cgc tgg	965
Arg Glu Thr Ser His Thr Val Leu Gly Ala Val Gly Glu Ala Arg Trp	
140 145 150 155	
aca tat gct gtc agc aaa ctc gcc gag gag cat atg gca tat gcc tat	1013
Thr Tyr Ala Val Ser Lys Leu Ala Glu Glu His Met Ala Tyr Ala Tyr	
160 165 170	
ttt aaa gaa ctt ggg ctt ccg acc gtc acc gtc cgc cct ttt aat gtt	1061
Phe Lys Glu Leu Gly Leu Pro Thr Val Thr Val Arg Pro Phe Asn Val	
175 180 185	
tat gga ccg gaa caa gtc ggc gaa ggc gcc atc aaa acg atg gtt cac	1109
Tyr Gly Pro Glu Gln Val Gly Glu Gly Ala Ile Lys Thr Met Val His	
190 195 200	
aga gct ctg tta gat gag ccg atc tat att cac ggc gat gga acg caa	1157
Arg Ala Leu Leu Asp Glu Pro Ile Tyr Ile His Gly Asp Gly Thr Gln	
205 210 215	
atc cgg gcc tgg tgt tac gta gat gac atg atc gac gga att ttg cgt	1205
Ile Arg Ala Trp Cys Tyr Val Asp Asp Met Ile Asp Gly Ile Leu Arg	
220 225 230 235	
tgt ttg acg atg aag gaa gcc atc gga gag tct ttc aac atc ggc aat	1253
Cys Leu Thr Met Lys Glu Ala Ile Gly Glu Ser Phe Asn Ile Gly Asn	
240 245 250	
gaa cgc act gtg atc acc gta tac gga ttg gca agc acg att atc aga	1301
Glu Arg Thr Val Ile Thr Val Tyr Gly Leu Ala Ser Thr Ile Ile Arg	
255 260 265	
gtt ctc gga tca aaa tca caa atc ttc ttt ggg gag aaa aaa gaa gcc	1349
Val Leu Gly Ser Lys Ser Gln Ile Phe Phe Gly Glu Lys Lys Glu Ala	
270 275 280	
gat att gaa ctg cgc atc cct cag gtc aat aaa gca aaa gag atg ctc	1397
Asp Ile Glu Leu Arg Ile Pro Gln Val Asn Lys Ala Lys Glu Met Leu	

285	290	295	
ggt ttc agc gct aaa gtt gat ctg gaa gaa ggc atc aga aga aca gct			1445
Gly Phe Ser Ala Lys Val Asp Leu Glu Glu Gly Ile Arg Arg Thr Ala			
300	305	310	315
gaa agc att aaa aaa aat ttg gat caa taagaaagga ggcgctattg			1492
Glu Ser Ile Lys Lys Asn Leu Asp Gln			
320			
ttgaaacaat ggaaaagcga aggaaaaggt gaattcactc tttcccagct tgggggctgt			1552
ggcgaaaatg tcgttatcga agacgggggtc cgcatttttc atccggaaaa catctatatc			1612
ggagataacg tttatatcgg ccatgacacg attttaaaag gctattataa gcatgacctg			1672
atcatcggtt caaacagctg gatcggggcag caatgtttta tacacggtgc cggcgggggtt			1732
acaatcggag aatttgcagg aattgggtccg aacgtccgga tacatgccgc ttaccatacc			1792
gatcctgata aacccgacag taccattttg ttttcgccgc ttacattcgc tcctattcat			1852
attgaagaaa actgcaacat cgggatcgggt gcgtctatcc tagcaggcgt tacgataggc			1912
gccactcca aaatcggagc aaatgccgtc gtcaatcgca atattccccc gtacagcata			1972
gca			1975

<210> 103  
 <211> 324  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 103

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Gly	Ala	Gly	Phe	Ile	Gly	Ser	Ser	Leu	Ile	Gly	Lys	Leu	Ile	Glu	Arg
		20						25					30		

Asn	Ser	Val	Thr	Val	Tyr	Asp	Asn	Phe	Ser	Arg	Asp	Ser	Leu	Arg	Tyr
		35					40					45			

Lys	Pro	Tyr	Arg	Asp	His	Pro	His	Leu	Lys	Val	Leu	Gln	Gly	Asp	Ile
	50					55					60				

Leu	Asp	Leu	Asn	Ala	Leu	Lys	Lys	Ala	Ile	Gln	Gly	Ala	Ser	His	Ile
65					70				75						80

Val His Ala Ala Gly Ile Ala Gly Ile Asp Thr Val Ile Gln Asn Pro

85					90					95					
Val	Lys	Thr	Met	Gln	Val	Asn	Met	Ile	Gly	Ser	Ala	Asn	Leu	Leu	Glu
			100					105					110		
Ala	Ala	Ala	Gly	Leu	Thr	Glu	Cys	Lys	Arg	Val	Val	Cys	Phe	Ser	Thr
			115				120					125			
Ser	Glu	Val	Phe	Gly	Gln	Ile	Ala	Phe	Arg	Ala	Arg	Glu	Thr	Ser	His
	130					135					140				
Thr	Val	Leu	Gly	Ala	Val	Gly	Glu	Ala	Arg	Trp	Thr	Tyr	Ala	Val	Ser
145						150					155				160
Lys	Leu	Ala	Glu	Glu	His	Met	Ala	Tyr	Ala	Tyr	Phe	Lys	Glu	Leu	Gly
				165					170					175	
Leu	Pro	Thr	Val	Thr	Val	Arg	Pro	Phe	Asn	Val	Tyr	Gly	Pro	Glu	Gln
			180					185					190		
Val	Gly	Glu	Gly	Ala	Ile	Lys	Thr	Met	Val	His	Arg	Ala	Leu	Leu	Asp
		195					200					205			
Glu	Pro	Ile	Tyr	Ile	His	Gly	Asp	Gly	Thr	Gln	Ile	Arg	Ala	Trp	Cys
	210					215					220				
Tyr	Val	Asp	Asp	Met	Ile	Asp	Gly	Ile	Leu	Arg	Cys	Leu	Thr	Met	Lys
225						230					235				240
Glu	Ala	Ile	Gly	Glu	Ser	Phe	Asn	Ile	Gly	Asn	Glu	Arg	Thr	Val	Ile
			245						250					255	
Thr	Val	Tyr	Gly	Leu	Ala	Ser	Thr	Ile	Ile	Arg	Val	Leu	Gly	Ser	Lys
			260					265					270		
Ser	Gln	Ile	Phe	Phe	Gly	Glu	Lys	Lys	Glu	Ala	Asp	Ile	Glu	Leu	Arg
		275					280					285			
Ile	Pro	Gln	Val	Asn	Lys	Ala	Lys	Glu	Met	Leu	Gly	Phe	Ser	Ala	Lys
	290					295					300				
Val	Asp	Leu	Glu	Glu	Gly	Ile	Arg	Arg	Thr	Ala	Glu	Ser	Ile	Lys	Lys
305						310					315				320

Asn Leu Asp Gln

<210> 104  
 <211> 1213  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(710)

<400> 104  
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 tggcaagcca gacgcttgaa agcatgtatg ccatcaacgc ggtcacgagc acgccggttt 120  
 tgcgcccttt aatcggcatg gataagacgg aaatcatcga aaaagcgaag gaaatcgata 180  
 cgtacgatat cagcatacgt ccgtacgaag actgctgcac gatctttacg ctttctgcgc 240  
 cgaaaacgcg tccgaaaaaa gagaaaatcg aacactttga aagctacaca gatttcgaac 300  
 cgcttatcaa cgaagctgtg gaaaacacgg aaacgattgt tttgagcagc aaagcggaaa 360  
 cgaaagatca atttgccgat tttttctaaa ggaatattca atcaaacatc tttgtctgtt 420  
 tttgcataca attaccaaac attctttgta tgaagtcatg tgttttttaca caatctatac 480  
 tcacaaggag gtgagaacac atg gct caa aac aac aga caa agc agt tct aac 533  
 Met Ala Gln Asn Asn Arg Gln Ser Ser Ser Asn  
 1 5 10  
 caa cta ttg gtt cct ggt gct gct caa gct atc gac caa atg aaa ttc 581  
 Gln Leu Leu Val Pro Gly Ala Ala Gln Ala Ile Asp Gln Met Lys Phe  
 15 20 25  
 gaa atc gct tct gaa ttt ggc gtt aac ctt gga gca gaa act act tct 629  
 Glu Ile Ala Ser Glu Phe Gly Val Asn Leu Gly Ala Glu Thr Thr Ser  
 30 35 40  
 cgt gca aac ggt tca gtt gga gga gaa atc act aag cgt tta gtt tct 677  
 Arg Ala Asn Gly Ser Val Gly Gly Glu Ile Thr Lys Arg Leu Val Ser  
 45 50 55  
 ttc gct caa cag caa atg ggt gga aca caa caa taattaaaat taaaaagcaa 730  
 Phe Ala Gln Gln Gln Met Gly Gly Thr Gln Gln  
 60 65 70  
 tggataatgg gtgggggttta atccccactc ttttttatgt tctgcaaaaat aggcatttcg 790  
 gaatacaatt gtatgaaagg attatgtata ataaaaagat ggcaacaagc aaggagatgg 850

aagggttgag aagagaagat ttgattgcg cggagaagta taatgcggtt gatgaaattg 910  
aaaaatttaa atcttcccgc gataagaccg cattgatctg ggaagatgaa tcagggcgtc 970  
aagtgtcatg gtcctatgaa aaattgattg aaaaggctta caaaatcggc agcatattga 1030  
cccgttctgg actgaaaaaa ggtgacaagc ttatcgtgat gatgccgcgg ataccggaaa 1090  
cgtatgccgt gtacatggcc attttaaaag ctggaatggt ggtcatccca tgttccgaaa 1150  
tgcttcgggc gaaagacttg gattacagga tcaagcatgc aggcgtcaaa ggagccgtcg 1210  
tat 1213

<210> 105  
<211> 70  
<212> PRT  
<213> Bacillus licheniformis

<400> 105

Met Ala Gln Asn Asn Arg Gln Ser Ser Ser Asn Gln Leu Leu Val Pro  
1 5 10 15

Gly Ala Ala Gln Ala Ile Asp Gln Met Lys Phe Glu Ile Ala Ser Glu  
20 25 30

Phe Gly Val Asn Leu Gly Ala Glu Thr Thr Ser Arg Ala Asn Gly Ser  
35 40 45

Val Gly Gly Glu Ile Thr Lys Arg Leu Val Ser Phe Ala Gln Gln Gln  
50 55 60

Met Gly Gly Thr Gln Gln  
65 70

<210> 106  
<211> 1196  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(695)

<400> 106  
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gatttttaaat acgattacag accgctccga tgatgtagtg agtccgctgc gcttttatga 120

aggggtatgcg cgggtccttg atcatgtgta ccagatcaaa gactatacgc tcaataaatc 180  
 ggcgcttgaa aaaatcgta ttgagcagac tggacagctc cgcgattttt ataaagatct 240  
 ggccgatccc gaatggaaca aagcgagaga catcacgcga gtcactgtgc tgtccgtcat 300  
 cgcttcgcac attcaggcga ccgcacattc catgattgac agcgtcttct taaaatatga 360  
 aatgaaataa tcgccgaccg gcgcgcctgg cttgcccaatt gccaggcggt tttttgcct 420  
 tcaacaattg ccagcataaa aagcctcagt ccaaatacaaa ctaaacaagc agtaccaatt 480  
 gaaaaaggag ttgagaatgc atg gca aga acg aat aag ctc ctc gtt ccc ggg 533  
   Met Ala Arg Thr Asn Lys Leu Leu Val Pro Gly  
   1  5  10  
 gca gag cag gtt tta gac cag ttc aaa tac gaa atc gcc caa gag ttc 581  
 Ala Glu Gln Val Leu Asp Gln Phe Lys Tyr Glu Ile Ala Gln Glu Phe  
   15  20  25  
 ggc gtc cag ctc ggc tcg gac tcg gtc gct cgc tca aac gga tct gta 629  
 Gly Val Gln Leu Gly Ser Asp Ser Val Ala Arg Ser Asn Gly Ser Val  
   30  35  40  
 ggc ggg gaa atg aca aaa cga ctt gta cag cag gca caa gct caa ttg 677  
 Gly Gly Glu Met Thr Lys Arg Leu Val Gln Gln Ala Gln Ala Gln Leu  
   45  50  55  
 aat ggg cat aat gac aaa taaataccct atggattatt cgccggggccc 725  
 Asn Gly His Asn Asp Lys  
 60  65  
 gctcggcgga tattcttggt tattcgtttg gtcagaaggc tttttctcct tttggttaagg 785  
 aagtgattta gagctctctt gatttgaacc ggaaccgctt tttggcgctt cttcctccgt 845  
 ctgctgaccg tctttgtcat tatggttatg ttcttgaggg tttttggtat taggggaatt 905  
 tgactccttt tctttttcca tttcttgatc aggttgagac tgatcttcat ctgaagggtt 965  
 ttgcgcgtcc ggatgatctt ccgtatctgc ttctttatca tccgtatgct gttccggctg 1025  
 atcttcttct ttcacagctt tctccttttc tctgtgttt tcttcctgat tttgatcatc 1085  
 ttttttattt tcattgtcat catctttgtt tttgtcttct aattcatctt tgtgggaacg 1145  
 gatataacgg cctgttgaga tgccttcttt ttgggctttt gcacgcgtat c 1196

<210> 107

<211> 65

<212> PRT

<213> Bacillus licheniformis

<400> 107

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Asp Gln Phe Lys Tyr Glu Ile Ala Gln Glu Phe Gly Val Gln Leu Gly			
20	25	30	
Ser Asp Ser Val Ala Arg Ser Asn Gly Ser Val Gly Gly Glu Met Thr			
35	40	45	
Lys Arg Leu Val Gln Gln Ala Gln Ala Gln Leu Asn Gly His Asn Asp			
50	55	60	

Lys  
65

<210> 108  
 <211> 2279  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501) .. (1463)

<400> 108  
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 agcggatatt gctgccatta tcaagaaatg caaaaacggc aggagcgaat atatcatcga 120  
 ccggcttgca ccgaatgaca gcgattatatt tttaatcaaa ccaaagcact cagcctttta 180  
 cggcactgct cttgaaacat tgctgcatga acttcatgtc gatcatttga tcatcactgg 240  
 gatcgcaggc aatatctgcg tattattttac ggcaaacgat gcttatatgc gggagtacga 300  
 gattacgatt ccgcgcgatt gcatcgctc aaacaatgaa aaagacaaca aatacgctt 360  
 gacgatgatg gaaaatgttc tgttcgccaa tatcacgacg gctaaggcga ttacctccga 420  
 aacttagagc atgaaacact tcctttcatc atatagtggg agcaatgaga aaggaggcgt 480  
 ttcccattca gatttatgtc gtg aaa aga ggc gat acc ctt tac caa atc gcg 533  
 Val Lys Arg Gly Asp Thr Leu Tyr Gln Ile Ala  
 1 5 10  
 aat cgt tac cga aca aca gtt aat gaa att gtc gcg acg aat gaa att 581  
 Asn Arg Tyr Arg Thr Thr Val Asn Glu Ile Val Ala Thr Asn Glu Ile  
 15 20 25  
 ccg aac ccg aat cgg ctt gtt gtc gga caa acc atc gtg atc ccg atc 629  
 Pro Asn Pro Asn Arg Leu Val Val Gly Gln Thr Ile Val Ile Pro Ile  
 30 35 40



gcc ggc gag ttt tat gag gtc aga cag gga gat aca tta gca tca atc Ala Gly Glu Phe Tyr Glu Val Arg Gln Gly Asp Thr Leu Ala Ser Ile 45 50 55	677
gga gca cgc ttt aat att tct ccg gct gaa ctg gcg agg atc aac cgc Gly Ala Arg Phe Asn Ile Ser Pro Ala Glu Leu Ala Arg Ile Asn Arg 60 65 70 75	725
att cag gtt agc gcc gtt tta ccg gtc gga ctg ctg ctt tac atc ccc Ile Gln Val Ser Ala Val Leu Pro Val Gly Leu Leu Leu Tyr Ile Pro 80 85 90	773
cct cgg cca aga cgg aac att gaa aca aac gcc tat atc gaa cct cgg Pro Arg Pro Arg Arg Asn Ile Glu Thr Asn Ala Tyr Ile Glu Pro Arg 95 100 105	821
gga gaa agc gta agc ccc gct ttg cag cag gcg gca aga gag gct tcg Gly Glu Ser Val Ser Pro Ala Leu Gln Gln Ala Ala Arg Glu Ala Ser 110 115 120	869
cca tac ttg acc tat ctg ggc gct ttc agc ttc cag gcg aag cgg gac Pro Tyr Leu Thr Tyr Leu Gly Ala Phe Ser Phe Gln Ala Lys Arg Asp 125 130 135	917
ggc aca ctc gaa gaa ccg ccg ctg aac aac tta aaa gaa att gcc gac Gly Thr Leu Glu Glu Pro Pro Leu Asn Asn Leu Lys Glu Ile Ala Asp 140 145 150 155	965
aga cat cgg act acg atg atg atg att gtc acc aat ctc gaa aat gaa Arg His Arg Thr Thr Met Met Met Ile Val Thr Asn Leu Glu Asn Glu 160 165 170	1013
gct ttc agc gac gaa ctc ggc agg atc att ctg acg gac cag aat gta Ala Phe Ser Asp Glu Leu Gly Arg Ile Ile Leu Thr Asp Gln Asn Val 175 180 185	1061
aaa aac aga ttg ctc gat aac atc gtt gca gcg gcc aga aga tac ggt Lys Asn Arg Leu Leu Asp Asn Ile Val Ala Ala Ala Arg Arg Tyr Gly 190 195 200	1109
ttt aaa gac atc cat ttt gac ttc gaa tac tta agg ccc gaa gat aga Phe Lys Asp Ile His Phe Asp Phe Glu Tyr Leu Arg Pro Glu Asp Arg 205 210 215	1157
gaa gcc tat aat cag ttt tta ccg gat gcc ccg gcc cgc ttc agg cag Glu Ala Tyr Asn Gln Phe Leu Arg Asp Ala Arg Ala Arg Phe Arg Gln 220 225 230 235	1205
gaa ggc tgg ctc atc tca acc gcg ctt gct ccg aaa acg aga gcg gat Glu Gly Trp Leu Ile Ser Thr Ala Leu Ala Pro Lys Thr Arg Ala Asp 240 245 250	1253
cag ccc gga caa tgg tat gaa gcc cat gat tac ccg gcc cac gcc gaa Gln Pro Gly Gln Trp Tyr Glu Ala His Asp Tyr Arg Ala His Gly Glu 255 260 265	1301

att gtc gat ttc gtc gtg ctg atg aca tat gag tgg ggc tac agc gga	1349
Ile Val Asp Phe Val Val Leu Met Thr Tyr Glu Trp Gly Tyr Ser Gly	
270 275 280	
ggg ccc ccg atg gcg gta tcg ccg atc ggg ccc gtc cgg gac gtg atc	1397
Gly Pro Pro Met Ala Val Ser Pro Ile Gly Pro Val Arg Asp Val Ile	
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gaa tac gca ctc acg gaa atg ccc gcc agc aaa atc gtc atg gga cag	1445
Glu Tyr Ala Leu Thr Glu Met Pro Ala Ser Lys Ile Val Met Gly Gln	
300 305 310 315	
aaa ctg tac ggc tat gac tgacgctccc ctatatgcac agcgggaccc	1493
Lys Leu Tyr Gly Tyr Asp	
320	
gttggccaag accaatccgg ccccaacggg gggattgaga tcgcgagcga gaacaatgcg	1553
gcgatacagt acgatgaaac agctcaggct ccaaacttcc gctatacggg caatgccggc	1613
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tggctcttga tagccgatca atttaatggt gttaaagaga cgttcccaag ttaaaggaac	1793
gttttttttc atggcagcgg atgatgatgt gatacaatat gtatggttca caaatgaatt	1853
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gcgcgggaaa aacaaccttg gccagcatgc tctccgaaaa gctctcactc tctttggtca	1973
aagaaatcgt cgaagaaaac ccttttcttg ataaatttta tgatgaaaaa gatgaatgga	2033
gctttcagct tgagatgttt ttcctctgca atcgctataa gcagcttgaa gataccgaga	2093
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ctttat	2279

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 <211> 321  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 109

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Thr Val Asn Glu Ile Val Ala Thr Asn Glu Ile Pro Asn Pro Asn Arg

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Leu Val Val Gly Gln Thr Ile Val Ile Pro Ile Ala Gly Glu Phe Tyr		
35	40	45
Glu Val Arg Gln Gly Asp Thr Leu Ala Ser Ile Gly Ala Arg Phe Asn		
50	55	60
Ile Ser Pro Ala Glu Leu Ala Arg Ile Asn Arg Ile Gln Val Ser Ala		
65	70	75
Val Leu Pro Val Gly Leu Leu Leu Tyr Ile Pro Pro Arg Pro Arg Arg		
85	90	95
Asn Ile Glu Thr Asn Ala Tyr Ile Glu Pro Arg Gly Glu Ser Val Ser		
100	105	110
Pro Ala Leu Gln Gln Ala Ala Arg Glu Ala Ser Pro Tyr Leu Thr Tyr		
115	120	125
Leu Gly Ala Phe Ser Phe Gln Ala Lys Arg Asp Gly Thr Leu Glu Glu		
130	135	140
Pro Pro Leu Asn Asn Leu Lys Glu Ile Ala Asp Arg His Arg Thr Thr		
145	150	155
Met Met Met Ile Val Thr Asn Leu Glu Asn Glu Ala Phe Ser Asp Glu		
165	170	175
Leu Gly Arg Ile Ile Leu Thr Asp Gln Asn Val Lys Asn Arg Leu Leu		
180	185	190
Asp Asn Ile Val Ala Ala Ala Arg Arg Tyr Gly Phe Lys Asp Ile His		
195	200	205
Phe Asp Phe Glu Tyr Leu Arg Pro Glu Asp Arg Glu Ala Tyr Asn Gln		
210	215	220
Phe Leu Arg Asp Ala Arg Ala Arg Phe Arg Gln Glu Gly Trp Leu Ile		
225	230	235
Ser Thr Ala Leu Ala Pro Lys Thr Arg Ala Asp Gln Pro Gly Gln Trp		
245	250	255

Tyr Glu Ala His Asp Tyr Arg Ala His Gly Glu Ile Val Asp Phe Val  
260 265 270

Val Leu Met Thr Tyr Glu Trp Gly Tyr Ser Gly Gly Pro Pro Met Ala  
275 280 285

Val Ser Pro Ile Gly Pro Val Arg Asp Val Ile Glu Tyr Ala Leu Thr  
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Glu Met Pro Ala Ser Lys Ile Val Met Gly Gln Lys Leu Tyr Gly Tyr  
305 310 315 320

Asp

<210> 110  
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<213> Bacillus licheniformis

<220>  
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aagaattatc cgcttcacgg ttctattcac cattccagct gtaaaaaacg gcgcatgatc 180  
cttctgcaac ggtcatagac atagcataaa accccctgtc acatacagag gaacaaaagg 240  
aagtgtgcc a g ttg ttt att tat aca gtc cag ccg gga gat tca cta ttt 290  
Leu Phe Ile Tyr Thr Val Gln Pro Gly Asp Ser Leu Phe  
1 5 10  
gtc atc ggc gcc aag ttc gga att tcg att gac cag atc cga ttg gcg 338  
Val Ile Gly Ala Lys Phe Gly Ile Ser Ile Asp Gln Ile Arg Leu Ala  
15 20 25  
aat ggg ttg atc gca aca aac att gtc ccc gga cag gct ctt tta ata 386  
Asn Gly Leu Ile Ala Thr Asn Ile Val Pro Gly Gln Ala Leu Leu Ile  
30 35 40 45  
ccg ctt tat aca tat acc gtt cag ccg gga gac agt tat tac acg att 434  
Pro Leu Tyr Thr Tyr Thr Val Gln Pro Gly Asp Ser Tyr Tyr Thr Ile  
50 55 60

gcc cgc cgg acg ttt gta tcc gtc gaa gca ttg caa aaa gca aat ccg	482
Ala Arg Arg Thr Phe Val Ser Val Glu Ala Leu Gln Lys Ala Asn Pro	
65 70 75	
tct gta acc cct tcc aat atg agg ccg ggg ata aaa gtg atg att ccg	530
Ser Val Thr Pro Ser Asn Met Arg Pro Gly Ile Lys Val Met Ile Pro	
80 85 90	
gaa ttg ccg aaa aaa ccg atc act gct tta gga tat tac aca ctg aga	578
Glu Leu Pro Lys Lys Pro Ile Thr Ala Leu Gly Tyr Tyr Thr Leu Arg	
95 100 105	
aac ccc cgg tta gac cag gaa ttg att cat aat ttt gcc cca tac gcc	626
Asn Pro Arg Leu Asp Gln Glu Leu Ile His Asn Phe Ala Pro Tyr Ala	
110 115 120 125	
acg tat ctg gca ttt ttt gaa tac cac att tca agc gac gga tcg tta	674
Thr Tyr Leu Ala Phe Phe Glu Tyr His Ile Ser Ser Asp Gly Ser Leu	
130 135 140	
agc gag ctg aat gat tca ccg gcc gta caa acg gct tgg aga cgg cgc	722
Ser Glu Leu Asn Asp Ser Pro Ala Val Gln Thr Ala Trp Arg Arg Arg	
145 150 155	
gtt cct ccc ctc atg aca gtc acc aat cta act gaa tca ggc ttc agt	770
Val Pro Pro Leu Met Thr Val Thr Asn Leu Thr Glu Ser Gly Phe Ser	
160 165 170	
ccg tct ctt gcg cac cgc gta tta aat cag cct gcc gta aga aat cgc	818
Pro Ser Leu Ala His Arg Val Leu Asn Gln Pro Ala Val Arg Asn Arg	
175 180 185	
ctc atc gac aat att gtc caa acg att tcc aga aaa gga tat gca ggc	866
Leu Ile Asp Asn Ile Val Gln Thr Ile Ser Arg Lys Gly Tyr Ala Gly	
190 195 200 205	
gtc aat att gat ttc gaa cag att ttg gag gaa gac aga gat tta ttt	914
Val Asn Ile Asp Phe Glu Gln Ile Leu Glu Glu Asp Arg Asp Leu Phe	
210 215 220	
tca ggt ttt ctc cgc ctg ttg aaa gag cgg ctg aag ccg tcc ggc tat	962
Ser Gly Phe Leu Arg Leu Leu Lys Glu Arg Leu Lys Pro Ser Gly Tyr	
225 230 235	
gtg ttg acg att gcc gtt ccg ccg aaa aca aat gaa aat atc gcc tgg	1010
Val Leu Thr Ile Ala Val Pro Pro Lys Thr Asn Glu Asn Ile Ala Trp	
240 245 250	
ctg aaa ggg tat gac tat ggc gga atc ggt gca gtg agc gac ctt atc	1058
Leu Lys Gly Tyr Asp Tyr Gly Gly Ile Gly Ala Val Ser Asp Leu Ile	
255 260 265	
ttc atc atg gca tac gac tgg cac cac ggg aca agc gag ccc ggc ccc	1106
Phe Ile Met Ala Tyr Asp Trp His His Gly Thr Ser Glu Pro Gly Pro	
270 275 280 285	
att gct ccg atc aat gaa gtc cgg caa aca att caa ttt gct ctc cgc	1154

Ile Ala Pro Ile Asn Glu Val Arg Gln Thr Ile Gln Phe Ala Leu Arg	
290 295 300	
cat gtc ccc aaa gaa aaa atc gtt ctc ggc ttt ccg ctt tac ggc tat	1202
His Val Pro Lys Glu Lys Ile Val Leu Gly Phe Pro Leu Tyr Gly Tyr	
305 310 315	
aac tgg acc ctg ccc tat cag ccc ggt gcc gta tac ccc gga atc gcc	1250
Asn Trp Thr Leu Pro Tyr Gln Pro Gly Ala Val Tyr Pro Gly Ile Ala	
320 325 330	
aac caa gac gcc gtt cag ctc gcc atg aag cac cag gca ccg att caa	1298
Asn Gln Asp Ala Val Gln Leu Ala Met Lys His Gln Ala Pro Ile Gln	
335 340 345	
tat gat aca aat tct gag tcc cct ttt ttc aga tac acc gat gaa cag	1346
Tyr Asp Thr Asn Ser Glu Ser Pro Phe Phe Arg Tyr Thr Asp Glu Gln	
350 355 360 365	
ggc aga cgg cat gtc gta tgg ttt gaa gac gca cgc agc atc gga aaa	1394
Gly Arg Arg His Val Val Trp Phe Glu Asp Ala Arg Ser Ile Gly Lys	
370 375 380	
aaa ctg cag ctg atc acc gaa tac gga ctt gac ggc ggc ggc gtc tgg	1442
Lys Leu Gln Leu Ile Thr Glu Tyr Gly Leu Asp Gly Gly Gly Val Trp	
385 390 395	
cag ctc aca ctc agt ttt ccg caa gga aca tgg ctc ttg acc aaa ttc	1490
Gln Leu Thr Leu Ser Phe Pro Gln Gly Thr Trp Leu Leu Thr Lys Phe	
400 405 410	
ttt cgc gtc cga aaa gtc tgacatcatt atgtgattta ttgtaaaata	1538
Phe Arg Val Arg Lys Val	
415	
acaaaccgaa taatcccgct aacgaatttt gatactaaag atgtgtcctt cacacaataa	1598
caaatttgaa aggaatgttt gcgattgaat aatgcgatcc atgaaacatt ggagctgcat	1658
gagctgttaa tgtttaaaaa cctttgtctg acaaagtcac caacaatgac gggaatgggt	1718
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gagcatttac aaggtctatt gtcagtgaga ggtgaaaccg tatgaacgaa ttcattccaaa	1838
acatgacagg catgggcgcg atgactgaac aagtcattgc caccgatttt ttaatctcgg	1898
caaaaaccgg tgtcaaaaac attgccacag ctatcacgga aacatcttct ccagaagtgc	1958
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<210> 111	
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<213> Bacillus licheniformis	

<400> 111

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Ile Ala Thr Asn Ile Val Pro Gly Gln Ala Leu Leu Ile Pro Leu Tyr  
35 40 45

Thr Tyr Thr Val Gln Pro Gly Asp Ser Tyr Tyr Thr Ile Ala Arg Arg  
50 55 60

Thr Phe Val Ser Val Glu Ala Leu Gln Lys Ala Asn Pro Ser Val Thr  
65 70 75 80

Pro Ser Asn Met Arg Pro Gly Ile Lys Val Met Ile Pro Glu Leu Pro  
85 90 95

Lys Lys Pro Ile Thr Ala Leu Gly Tyr Tyr Thr Leu Arg Asn Pro Arg  
100 105 110

Leu Asp Gln Glu Leu Ile His Asn Phe Ala Pro Tyr Ala Thr Tyr Leu  
115 120 125

Ala Phe Phe Glu Tyr His Ile Ser Ser Asp Gly Ser Leu Ser Glu Leu  
130 135 140

Asn Asp Ser Pro Ala Val Gln Thr Ala Trp Arg Arg Arg Val Pro Pro  
145 150 155 160

Leu Met Thr Val Thr Asn Leu Thr Glu Ser Gly Phe Ser Pro Ser Leu  
165 170 175

Ala His Arg Val Leu Asn Gln Pro Ala Val Arg Asn Arg Leu Ile Asp  
180 185 190

Asn Ile Val Gln Thr Ile Ser Arg Lys Gly Tyr Ala Gly Val Asn Ile  
195 200 205

Asp Phe Glu Gln Ile Leu Glu Glu Asp Arg Asp Leu Phe Ser Gly Phe  
210 215 220

Leu Arg Leu Leu Lys Glu Arg Leu Lys Pro Ser Gly Tyr Val Leu Thr  
 225 230 235 240

Ile Ala Val Pro Pro Lys Thr Asn Glu Asn Ile Ala Trp Leu Lys Gly  
 245 250 255

Tyr Asp Tyr Gly Gly Ile Gly Ala Val Ser Asp Leu Ile Phe Ile Met  
 260 265 270

Ala Tyr Asp Trp His His Gly Thr Ser Glu Pro Gly Pro Ile Ala Pro  
 275 280 285

Ile Asn Glu Val Arg Gln Thr Ile Gln Phe Ala Leu Arg His Val Pro  
 290 295 300

Lys Glu Lys Ile Val Leu Gly Phe Pro Leu Tyr Gly Tyr Asn Trp Thr  
 305 310 315 320

Leu Pro Tyr Gln Pro Gly Ala Val Tyr Pro Gly Ile Ala Asn Gln Asp  
 325 330 335

Ala Val Gln Leu Ala Met Lys His Gln Ala Pro Ile Gln Tyr Asp Thr  
 340 345 350

Asn Ser Glu Ser Pro Phe Phe Arg Tyr Thr Asp Glu Gln Gly Arg Arg  
 355 360 365

His Val Val Trp Phe Glu Asp Ala Arg Ser Ile Gly Lys Lys Leu Gln  
 370 375 380

Leu Ile Thr Glu Tyr Gly Leu Asp Gly Gly Gly Val Trp Gln Leu Thr  
 385 390 395 400

Leu Ser Phe Pro Gln Gly Thr Trp Leu Leu Thr Lys Phe Phe Arg Val  
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Arg Lys Val

<210> 112

<211> 2014

<212> DNA

<213> Bacillus licheniformis



<220>

<221> CDS

<222> (558) .. (1511)

<400> 112

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catggccgaa aaaatatagc attccccttc cgcccgtcc atggctgtgt acataccggc	180
aagcggccct ttcctctgt acgggtcgat atcttcacgc accgcttttt tcccaggttc	240
tataaaccgc tccgtcaagc ccggacggct caatatcagg acgtcgtctc ccagcgctg	300
tttgaccat tgataaagcg gcttgccctt ccagcgggca aacgccttcg gttccccaaa	360
acggcgcgaa agccccctg ataatatgac atgtatttct ttcatacggc tcaaccttcc	420
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atagggggct ggtcacc atg aaa aaa aca tcg ggt tcg ctg cct tat ttt	590
Met Lys Lys Thr Ser Gly Ser Leu Pro Tyr Phe	
1 5 10	
caa gat tta tca cag gaa aac ctt ttt tta aaa gct gag ctg gca aga	638
Gln Asp Leu Ser Gln Glu Asn Leu Phe Leu Lys Ala Glu Leu Ala Arg	
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tca cat caa ttg ata cac gag ctt gaa gca agc tat ttt cac cag aaa	686
Ser His Gln Leu Ile His Glu Leu Glu Ala Ser Tyr Phe His Gln Lys	
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aat cat aag ctc agc cgg gaa aac gca gca atg aaa cag cag ctt cag	734
Asn His Lys Leu Ser Arg Glu Asn Ala Ala Met Lys Gln Gln Leu Gln	
45 50 55	
cag ctg tca ttc gaa ctg gag cgg att tcg gca aac aag gaa gac aag	782
Gln Leu Ser Phe Glu Leu Glu Arg Ile Ser Ala Asn Lys Glu Asp Lys	
60 65 70 75	
tcg gcc gaa acg ctc aac cgg ata aaa agc gaa ttg ctg agt aaa atc	830
Ser Ala Glu Thr Leu Asn Arg Ile Lys Ser Glu Leu Leu Ser Lys Ile	
80 85 90	
gtc gtt ctt cag gag ctt ctt caa aaa gaa acc tat gca aga aaa caa	878
Val Val Leu Gln Glu Leu Leu Gln Lys Glu Thr Tyr Ala Arg Lys Gln	
95 100 105	
gag ata gaa gaa aag cac cgc ctt cat tta aca aat gta aaa gcc gaa	926
Glu Ile Glu Glu Lys His Arg Leu His Leu Thr Asn Val Lys Ala Glu	
110 115 120	

gaa gag aaa aaa agc tta cat agc caa ata gaa tac gaa aag ctt cat Glu Glu Lys Lys Ser Leu His Ser Gln Ile Glu Tyr Glu Lys Leu His 125 130 135	974
gca gaa aga gaa aaa acg ctg agg gaa aaa aag gaa cag gag ctc aaa Ala Glu Arg Glu Lys Thr Leu Arg Glu Lys Lys Glu Gln Glu Leu Lys 140 145 150 155	1022
aac gct gca tac gaa aat gcc cgc ctg aaa gat gaa ctt cat gct aaa Asn Ala Ala Tyr Glu Asn Ala Arg Leu Lys Asp Glu Leu His Ala Lys 160 165 170	1070
agt ctt cag ctc aaa caa atc gaa act gat gtt gcg gta tta aaa gag Ser Leu Gln Leu Lys Gln Ile Glu Thr Asp Val Ala Val Leu Lys Glu 175 180 185	1118
cgg gtg acg gaa acg aaa agc cgg ctt ttg gag gct gaa aaa aca aaa Arg Val Thr Glu Thr Lys Ser Arg Leu Leu Glu Ala Glu Lys Thr Lys 190 195 200	1166
gaa gcg ctg ttt tat gaa acg att ctc tct tat aaa agg caa ctc gat Glu Ala Leu Phe Tyr Glu Thr Ile Leu Ser Tyr Lys Arg Gln Leu Asp 205 210 215	1214
gaa agt gat aag tgg atc gct tct cat ttt gcc gat att gat gca ttt Glu Ser Asp Lys Trp Ile Ala Ser His Phe Ala Asp Ile Asp Ala Phe 220 225 230 235	1262
cag cag acg gag aag gcg ctt gaa caa aac gag gag gtt ttt gaa cgg Gln Gln Thr Glu Lys Ala Leu Glu Gln Asn Glu Glu Val Phe Glu Arg 240 245 250	1310
aca gaa cag atc gag gcg gtg ctt caa act gtt aca gag caa gtt gat Thr Glu Gln Ile Glu Ala Val Leu Gln Thr Val Thr Glu Gln Val Asp 255 260 265	1358
cag ctc caa caa caa ttg agc gcc att caa caa aat tat acg aaa atg Gln Leu Gln Gln Gln Leu Ser Ala Ile Gln Gln Asn Tyr Thr Lys Met 270 275 280	1406
gat caa aaa ata aca gaa tgg aaa aaa cag gcg aaa gaa gaa aca ccc Asp Gln Lys Ile Thr Glu Trp Lys Lys Gln Ala Lys Glu Glu Thr Pro 285 290 295	1454
ccg caa aaa tgg gtc tat caa att aaa cgc aaa gac aaa gaa aca aaa Pro Gln Lys Trp Val Tyr Gln Ile Lys Arg Lys Asp Lys Glu Thr Lys 300 305 310 315	1502
cct tta aat taaataccac tttaaggaat aatttggttt ttacaaaaaa Pro Leu Asn	1551
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<211> 318  
<212> PRT  
<213> Bacillus licheniformis

<400> 113

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His Glu Leu Glu Ala Ser Tyr Phe His Gln Lys Asn His Lys Leu Ser  
35 40 45

Arg Glu Asn Ala Ala Met Lys Gln Gln Leu Gln Gln Leu Ser Phe Glu  
50 55 60

Leu Glu Arg Ile Ser Ala Asn Lys Glu Asp Lys Ser Ala Glu Thr Leu  
65 70 75 80

Asn Arg Ile Lys Ser Glu Leu Leu Ser Lys Ile Val Val Leu Gln Glu  
85 90 95

Leu Leu Gln Lys Glu Thr Tyr Ala Arg Lys Gln Glu Ile Glu Glu Lys  
100 105 110

His Arg Leu His Leu Thr Asn Val Lys Ala Glu Glu Glu Lys Lys Ser  
115 120 125

Leu His Ser Gln Ile Glu Tyr Glu Lys Leu His Ala Glu Arg Glu Lys  
130 135 140

Thr Leu Arg Glu Lys Lys Glu Gln Glu Leu Lys Asn Ala Ala Tyr Glu  
145 150 155 160

Asn Ala Arg Leu Lys Asp Glu Leu His Ala Lys Ser Leu Gln Leu Lys  
165 170 175

Gln Ile Glu Thr Asp Val Ala Val Leu Lys Glu Arg Val Thr Glu Thr  
180 185 190

Lys Ser Arg Leu Leu Glu Ala Glu Lys Thr Lys Glu Ala Leu Phe Tyr  
195 200 205

Glu Thr Ile Leu Ser Tyr Lys Arg Gln Leu Asp Glu Ser Asp Lys Trp  
210 215 220

Ile Ala Ser His Phe Ala Asp Ile Asp Ala Phe Gln Gln Thr Glu Lys  
225 230 235 240

Ala Leu Glu Gln Asn Glu Glu Val Phe Glu Arg Thr Glu Gln Ile Glu  
245 250 255

Ala Val Leu Gln Thr Val Thr Glu Gln Val Asp Gln Leu Gln Gln Gln  
260 265 270

Leu Ser Ala Ile Gln Gln Asn Tyr Thr Lys Met Asp Gln Lys Ile Thr  
275 280 285

Glu Trp Lys Lys Gln Ala Lys Glu Glu Thr Pro Pro Gln Lys Trp Val  
290 295 300

Tyr Gln Ile Lys Arg Lys Asp Lys Glu Thr Lys Pro Leu Asn  
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<210> 114  
<211> 2341  
<212> DNA  
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<220>  
<221> CDS  
<222> (501)..(1838)

<400> 114  
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agccccgttct aaacggcagc atcgagaaaa aagcagaccg cgaatcagtg gaagctgtgg 180  
aagaagcggg agatcaaaat aaaaaagaaa cagaagcttt atttttctat aatccccgaca 240  
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tcaattttca attaaaaaga aaataatttt tagacttgtc tcatatgatg ggataaaccc 480  
gtgagacaag gagagacctc atg aac cgt ttt gta aaa gga atc gtt ctt ctt 533  
Met Asn Arg Phe Val Lys Gly Ile Val Leu Leu  
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tcg cta gct gct ttt ttt gca gaa tgt ctt gaa ttc gtc atc aac atg 581  
Ser Leu Ala Ala Phe Phe Ala Glu Cys Leu Glu Phe Val Ile Asn Met  
15 20 25  
att ctt gca cgg gag ctt ggc gag cat ggc atg ggg ctc tac atg agt 629  
Ile Leu Ala Arg Glu Leu Gly Glu His Gly Met Gly Leu Tyr Met Ser  
30 35 40  
gtt ttg cct tcc att ttt ttg gtc gtg gtg att gcg agc ctt gag ctg 677  
Val Leu Pro Ser Ile Phe Leu Val Val Val Ile Ala Ser Leu Glu Leu  
45 50 55  
ccc gta tca ata tcg aag ttt atc gcc gag tcc aac ccg aag ctg cac 725  
Pro Val Ser Ile Ser Lys Phe Ile Ala Glu Ser Asn Pro Lys Leu His  
60 65 70 75  
gaa agc atg ctg aaa cat gca ttg cgg atg act gcg gtc tgc acg gtt 773  
Glu Ser Met Leu Lys His Ala Leu Arg Met Thr Ala Val Cys Thr Val  
80 85 90  
ttc tcc acg gca gcc gca gtg atc att ctt cca ttt att ccg gtt ttt 821  
Phe Ser Thr Ala Ala Ala Val Ile Ile Leu Pro Phe Ile Pro Val Phe  
95 100 105  
gat tct tac cac cct cta atc aga gga ctt gtg atc ggg atg att cct 869  
Asp Ser Tyr His Pro Leu Ile Arg Gly Leu Val Ile Gly Met Ile Pro  
110 115 120  
acg gtt gca ttc aca tcg atc gcg aga ggc tac ttc atg ggc gtt cag 917  
Thr Val Ala Phe Thr Ser Ile Ala Arg Gly Tyr Phe Met Gly Val Gln  
125 130 135  
caa atg ggt aaa atc gca acg gcg aat gcc ttg aaa aaa atc ttt cag 965  
Gln Met Gly Lys Ile Ala Thr Ala Asn Ala Leu Lys Lys Ile Phe Gln  
140 145 150 155  
ctc atc ggc ttg ttt tta ttt ttt caa tgg tat tcc ttt gaa ttg gat 1013  
Leu Ile Gly Leu Phe Leu Phe Phe Gln Trp Tyr Ser Phe Glu Leu Asp  
160 165 170  
act tct ctt ctc att tca ttg ttt gtc ctc gtt gca agt gaa gtg gtc 1061

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Val	Phe	Val	Tyr	Leu	Phe	Ser	Gln	Phe	Val	Leu	Val	Arg	Arg	Ala	Ala		
		190					195					200					
caa	aaa	ggg	cag	cag	atc	cac	ttg	cgg	aga	aac	gat	gtt	tta	aaa	cgc	1157	
Gln	Lys	Gly	Gln	Gln	Ile	His	Leu	Arg	Arg	Asn	Asp	Val	Leu	Lys	Arg		
	205					210					215						
ctg	ctc	act	gtt	tcg	atc	ccg	acg	acg	ggg	ctg	cgc	gtg	ttt	cat	gct	1205	
Leu	Leu	Thr	Val	Ser	Ile	Pro	Thr	Thr	Gly	Leu	Arg	Val	Phe	His	Ala		
220					225					230					235		
gtg	aca	aat	gcc	gtc	gaa	cct	ttt	ttg	gtg	aag	ggg	acg	ctg	ctt	gcc	1253	
Val	Thr	Asn	Ala	Val	Glu	Pro	Phe	Leu	Val	Lys	Gly	Thr	Leu	Leu	Ala		
				240					245					250			
gct	ggc	gta	tca	aga	aca	tcg	gcc	atc	gac	cag	ttc	ggc	atg	ctt	tcg	1301	
Ala	Gly	Val	Ser	Arg	Thr	Ser	Ala	Ile	Asp	Gln	Phe	Gly	Met	Leu	Ser		
			255					260					265				
gga	gtt	gcg	atg	aca	atc	ggc	ttt	ttt	ccg	gct	ttt	atc	gcc	cat	tca	1349	
Gly	Val	Ala	Met	Thr	Ile	Gly	Phe	Phe	Pro	Ala	Phe	Ile	Ala	His	Ser		
		270					275					280					
ctg	atg	gtc	gtc	atg	atc	ccg	agc	att	tct	gaa	agc	tac	gct	tac	ggg	1397	
Leu	Met	Val	Val	Met	Ile	Pro	Ser	Ile	Ser	Glu	Ser	Tyr	Ala	Tyr	Gly		
	285					290					295						
caa	tac	gaa	aga	gtg	atc	aaa	cgg	att	aaa	cag	gcg	atc	ttt	att	acg	1445	
Gln	Tyr	Glu	Arg	Val	Ile	Lys	Arg	Ile	Lys	Gln	Ala	Ile	Phe	Ile	Thr		
300					305					310					315		
ctg	ttt	tac	ggc	ata	ccg	tcc	gtc	atg	gtg	atg	tat	cac	ttt	gca	gag	1493	
Leu	Phe	Tyr	Gly	Ile	Pro	Ser	Val	Met	Val	Met	Tyr	His	Phe	Ala	Glu		
				320					325					330			
ccg	ctg	acc	cat	tta	ttt	ttc	gat	tcg	gtc	aag	gcg	tcg	ttt	tac	ctt	1541	
Pro	Leu	Thr	His	Leu	Phe	Phe	Asp	Ser	Val	Lys	Ala	Ser	Phe	Tyr	Leu		
			335					340					345				
aaa	atg	ttg	tgg	ccg	tat	ttt	tta	ttc	cac	ttt	ttt	gcg	atg	cct	ttt	1589	
Lys	Met	Leu	Trp	Pro	Tyr	Phe	Leu	Phe	His	Phe	Phe	Ala	Met	Pro	Phe		
		350					355					360					
cag	gcc	tgt	tta	atc	gga	atg	ggg	ttg	gcc	aaa	gat	gct	ttt	tat	cat	1637	
Gln	Ala	Cys	Leu	Ile	Gly	Met	Gly	Leu	Ala	Lys	Asp	Ala	Phe	Tyr	His		
	365					370					375						
aac	gtt	tgg	gcc	agt	gtc	tta	tcg	ttt	ttg	atg	atg	tat	gtt	ctc	ggg	1685	
Asn	Val	Trp	Ala	Ser	Val	Leu	Ser	Phe	Leu	Met	Met	Tyr	Val	Leu	Gly		
380					385					390					395		
tcc	atg	cag	act	ttg	cag	atg	acg	ggg	atc	att	ctt	gcg	atg	aat	acc	1733	
Ser	Met	Gln	Thr	Leu	Gln	Met	Thr	Gly	Ile	Ile	Leu	Ala	Met	Asn	Thr		

400	405	410	
ggt atg att ttg ctg acg gcg ctg cat tat gtg acg att tgc aag gag			1781
Gly Met Ile Leu Leu Thr Ala Leu His Tyr Val Thr Ile Cys Lys Glu			
415	420	425	
ctg ggc gtc acg ctt ttt ttg aca aac aaa tcc cga tct ccg aga att			1829
Leu Gly Val Thr Leu Phe Leu Thr Asn Lys Ser Arg Ser Pro Arg Ile			
430	435	440	
gaa agc cgc tgatggatcc tcttcatagt tttagctttt gcggggaagc			1878
Glu Ser Arg			
445			
taatattaaa aaagaagggg agttcccatg cgaagaatca gtctcattta cccgctcatc			1938
ctgctgtttt ttaccggggtt attcgtattt cagccgcagg catctgcaaa acaagcttcg			1998
ccggcagtca tgcagatgaa cacggtcgaa ggtcagcgcg tcgtcattcc cgccgaaggc			2058
cagaagacga tcgttcattt ttggacgacc tgggtcccg c catgccgtga agagcttccg			2118
cgattccaat cctactatga aagcaagcaa tccggcgtca agctcgtgac cgttaattta			2178
ctgaatgccg aaaagaacga acagaaggta aaacagttta ttaaagcaaa caagctgaca			2238
tttccgatcg tttttgacaa aaaggggtgag atgatgaaag catataaagt catgacaatt			2298
cctacgactt ttttctttaa tgaaaaagga gagctggaga aaa			2341
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20 25 30			
Leu Gly Glu His Gly Met Gly Leu Tyr Met Ser Val Leu Pro Ser Ile			
35 40 45			
Phe Leu Val Val Val Ile Ala Ser Leu Glu Leu Pro Val Ser Ile Ser			
50 55 60			
Lys Phe Ile Ala Glu Ser Asn Pro Lys Leu His Glu Ser Met Leu Lys			
65 70 75 80			

His Ala Leu Arg Met Thr Ala Val Cys Thr Val Phe Ser Thr Ala Ala  
85 90 95

Ala Val Ile Ile Leu Pro Phe Ile Pro Val Phe Asp Ser Tyr His Pro  
100 105 110

Leu Ile Arg Gly Leu Val Ile Gly Met Ile Pro Thr Val Ala Phe Thr  
115 120 125

Ser Ile Ala Arg Gly Tyr Phe Met Gly Val Gln Gln Met Gly Lys Ile  
130 135 140

Ala Thr Ala Asn Ala Leu Lys Lys Ile Phe Gln Leu Ile Gly Leu Phe  
145 150 155 160

Leu Phe Phe Gln Trp Tyr Ser Phe Glu Leu Asp Thr Ser Leu Leu Ile  
165 170 175

Ser Leu Phe Val Leu Val Ala Ser Glu Val Val Val Phe Val Tyr Leu  
180 185 190

Phe Ser Gln Phe Val Leu Val Arg Arg Ala Ala Gln Lys Gly Gln Gln  
195 200 205

Ile His Leu Arg Arg Asn Asp Val Leu Lys Arg Leu Leu Thr Val Ser  
210 215 220

Ile Pro Thr Thr Gly Leu Arg Val Phe His Ala Val Thr Asn Ala Val  
225 230 235 240

Glu Pro Phe Leu Val Lys Gly Thr Leu Leu Ala Ala Gly Val Ser Arg  
245 250 255

Thr Ser Ala Ile Asp Gln Phe Gly Met Leu Ser Gly Val Ala Met Thr  
260 265 270

Ile Gly Phe Phe Pro Ala Phe Ile Ala His Ser Leu Met Val Val Met  
275 280 285

Ile Pro Ser Ile Ser Glu Ser Tyr Ala Tyr Gly Gln Tyr Glu Arg Val  
290 295 300



Ile Lys Arg Ile Lys Gln Ala Ile Phe Ile Thr Leu Phe Tyr Gly Ile  
 305 310 315 320

Pro Ser Val Met Val Met Tyr His Phe Ala Glu Pro Leu Thr His Leu  
 325 330 335

Phe Phe Asp Ser Val Lys Ala Ser Phe Tyr Leu Lys Met Leu Trp Pro  
 340 345 350

Tyr Phe Leu Phe His Phe Phe Ala Met Pro Phe Gln Ala Cys Leu Ile  
 355 360 365

Gly Met Gly Leu Ala Lys Asp Ala Phe Tyr His Asn Val Trp Ala Ser  
 370 375 380

Val Leu Ser Phe Leu Met Met Tyr Val Leu Gly Ser Met Gln Thr Leu  
 385 390 395 400

Gln Met Thr Gly Ile Ile Leu Ala Met Asn Thr Gly Met Ile Leu Leu  
 405 410 415

Thr Ala Leu His Tyr Val Thr Ile Cys Lys Glu Leu Gly Val Thr Leu  
 420 425 430

Phe Leu Thr Asn Lys Ser Arg Ser Pro Arg Ile Glu Ser Arg  
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<210> 116

<211> 1417

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (420) .. (914)

<400> 116

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tgaggtgaca atcggaatgc cgcctgggt gatcgctca atatcccgat aaatcgttct 120

gacagagact tgaacatgc cggcaagctc ctttgctgc acttggcggt tattaatcaa 180

taaaatcaca atggccaaaa gccggtcaat tttcactgca gatccctcac attcatcttg 240

tgcagcctct ttttttctgc tatttttcatt ccatagcgca caccattctg ggatatcatg 300

acaaaaaaga ggatctcatc acccatttat ctagaaaacc acttttcagg ttacgatttg 360  
 tacagtttgg acatatactc cttaaaaaag gaggttttaa aaacatcata ttttatttt 419  
 ttg cag ttt ttc atc att gtg tcc atc gtc tat atc aag ttc aaa cgg 467  
 Leu Gln Phe Phe Ile Ile Val Ser Ile Val Tyr Ile Lys Phe Lys Arg  
 1 5 10 15  
 tcg gtc ggt tat cag cct tta aag ccg gca cgc atg ttg ttc cgg atc 515  
 Ser Val Gly Tyr Gln Pro Leu Lys Pro Ala Arg Met Leu Phe Arg Ile  
 20 25 30  
 atc ctt ttt tcg gga att ttc gtt ttt ctg ctg acg atg agc gca ctt 563  
 Ile Leu Phe Ser Gly Ile Phe Val Phe Leu Leu Thr Met Ser Ala Leu  
 35 40 45  
 cac cct tta tca tac ttt tat gat ctg att ggg atc gcg ctc gga ctc 611  
 His Pro Leu Ser Tyr Phe Tyr Asp Leu Ile Gly Ile Ala Leu Gly Leu  
 50 55 60  
 atc ttg acc gtc tat gcg ctg aag cat gtg tcg atc gaa aat cgg ggc 659  
 Ile Leu Thr Val Tyr Ala Leu Lys His Val Ser Ile Glu Asn Arg Gly  
 65 70 75 80  
 gga gtc ctt tat ttc aga acg cat tta tgg gtt gaa ttg atc gta ctc 707  
 Gly Val Leu Tyr Phe Arg Thr His Leu Trp Val Glu Leu Ile Val Leu  
 85 90 95  
 ttt tta ttt tta tac cgg ttt ctg tac cgg atc gcc gag atc ggc cag 755  
 Phe Leu Phe Leu Tyr Arg Phe Leu Tyr Arg Ile Ala Glu Ile Gly Gln  
 100 105 110  
 ctg cag act gcg gtt tca gac ggg ggt tcg gca gct tac ggc gcc ctt 803  
 Leu Gln Thr Ala Val Ser Asp Gly Gly Ser Ala Ala Tyr Gly Ala Leu  
 115 120 125  
 ttt gcg cag gac ccg gcg acg atg atc ggt ttt ttt gta ctg gcc gtt 851  
 Phe Ala Gln Asp Pro Ala Thr Met Ile Gly Phe Phe Val Leu Ala Val  
 130 135 140  
 tat tat gtc ggt ttc tct ttt ttt gtt tta aaa aaa ggc aga acc gaa 899  
 Tyr Tyr Val Gly Phe Ser Phe Phe Val Leu Lys Lys Gly Arg Thr Glu  
 145 150 155 160  
 gaa aag cgc tca gct taaaaaggca aactcgggaa attgagtttg ccttttaaac 954  
 Glu Lys Arg Ser Ala  
 165  
 tttagtcatg ttgtgtatga tcgatcatct gctgaagtac atcgaggaca tgctggtcct 1014  
 ccggagaata aaaaatggaa gtccctgccc ttcttgattt gacgagacga aggtttttta 1074  
 aaaacctgag ctggtgagaa acggttgact gcaggagact cagcttctct gctatttcat 1134  
 taaccgaatg ctcgccttgt gagagcaggt gaagaatttt gattctcggt gggtcagaga 1194  
 gcgctttaaa cgtctgtgaa acgagaaata aagtttcttc atctaactcg gcccgcacct 1254

gtttttctgt tgttttcttga ttgtgctcac tcatgctttt caccttttcc gcgcgacttt 1314  
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 <211> 165  
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 <213> Bacillus licheniformis

<400> 117

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Ser Val Gly Tyr Gln Pro Leu Lys Pro Ala Arg Met Leu Phe Arg Ile  
 20 25 30

Ile Leu Phe Ser Gly Ile Phe Val Phe Leu Leu Thr Met Ser Ala Leu  
 35 40 45

His Pro Leu Ser Tyr Phe Tyr Asp Leu Ile Gly Ile Ala Leu Gly Leu  
 50 55 60

Ile Leu Thr Val Tyr Ala Leu Lys His Val Ser Ile Glu Asn Arg Gly  
 65 70 75 80

Gly Val Leu Tyr Phe Arg Thr His Leu Trp Val Glu Leu Ile Val Leu  
 85 90 95

Phe Leu Phe Leu Tyr Arg Phe Leu Tyr Arg Ile Ala Glu Ile Gly Gln  
 100 105 110

Leu Gln Thr Ala Val Ser Asp Gly Gly Ser Ala Ala Tyr Gly Ala Leu  
 115 120 125

Phe Ala Gln Asp Pro Ala Thr Met Ile Gly Phe Phe Val Leu Ala Val  
 130 135 140

Tyr Tyr Val Gly Phe Ser Phe Phe Val Leu Lys Lys Gly Arg Thr Glu  
 145 150 155 160

Glu Lys Arg Ser Ala  
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<210> 118  
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 <213> Bacillus licheniformis

<220>  
 <221> CDS  
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 cggagaaccg tatgacggcc aggttgccgt tgcagctgtt atattaaaca ggctcgatag 240  
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 cgcggacgga cagatttata tgacgccgga tgaaacggcg aaaaaagccg ttcttgacgc 360  
 catcaacggc tgggatccat cagaaaaatgc cacttactat tttaaccctg acacggccac 420  
 tagctcatgg atttggggca gacctcaaat taaaaggatc ggtaaacaca ttttctgtga 480  
 ataaaagcga ggtgctataa atg atc aga gga att tta atc gcc ctt tta ggt 533  
 Met Ile Arg Gly Ile Leu Ile Ala Leu Leu Gly  
 1 5 10  
 gtc gcc atc gtc gga aca agc tat tgg ggc tat aaa gaa cat cag gag 581  
 Val Ala Ile Val Gly Thr Ser Tyr Trp Gly Tyr Lys Glu His Gln Glu  
 15 20 25  
 aaa gac gcc gtt ttg ctt cat gcc gaa aac aac tat caa agg gca ttt 629  
 Lys Asp Ala Val Leu Leu His Ala Glu Asn Asn Tyr Gln Arg Ala Phe  
 30 35 40  
 cac gac tta act tat cag gtg gat cag ctg cat gat aaa atc ggg agc 677  
 His Asp Leu Thr Tyr Gln Val Asp Gln Leu His Asp Lys Ile Gly Ser  
 45 50 55  
 acg ctt gcg atg aac agc aaa aaa acg ctg tct ccc gct ttg gcg gaa 725  
 Thr Leu Ala Met Asn Ser Lys Lys Thr Leu Ser Pro Ala Leu Ala Glu  
 60 65 70 75  
 gtc tgg aaa acg act tct gaa gcg cat aac aat gtc agc cag ctg ccg 773  
 Val Trp Lys Thr Thr Ser Glu Ala His Asn Asn Val Ser Gln Leu Pro  
 80 85 90  
 ctg acc tta atg ccg ttt aac aag acc gaa gag ttt ttg gca aag gtc 821  
 Leu Thr Leu Met Pro Phe Asn Lys Thr Glu Glu Phe Leu Ala Lys Val  
 95 100 105

gga gat ttc agc tac aaa gca gcc gtg cgc gat ctt gac aaa gag ccg	869
Gly Asp Phe Ser Tyr Lys Ala Ala Val Arg Asp Leu Asp Lys Glu Pro	
110 115 120	
ctc aat aaa aaa gag tac gct tct tta aat cag cta tat gaa aat tca	917
Leu Asn Lys Lys Glu Tyr Ala Ser Leu Asn Gln Leu Tyr Glu Asn Ser	
125 130 135	
aag gat ata caa aat gaa ctg cgt aat gtc cag cat ttg att att gac	965
Lys Asp Ile Gln Asn Glu Leu Arg Asn Val Gln His Leu Ile Ile Asp	
140 145 150 155	
aaa aat ttg aga tgg atg gat gta gaa ctt gcg ctc gcg tcc ggc caa	1013
Lys Asn Leu Arg Trp Met Asp Val Glu Leu Ala Leu Ala Ser Gly Gln	
160 165 170	
aaa caa agc gac aat aag att att aat ggc ttt aaa acc gtt gaa aaa	1061
Lys Gln Ser Asp Asn Lys Ile Ile Asn Gly Phe Lys Thr Val Glu Lys	
175 180 185	
agc gca agt gca ttt tcg gat acg gat tta ggc gcg aca gag atg acg	1109
Ser Ala Ser Ala Phe Ser Asp Thr Asp Leu Gly Ala Thr Glu Met Thr	
190 195 200	
aac acg aaa aaa gag cag caa ggg tac gac cat tta caa ggc aaa aga	1157
Asn Thr Lys Lys Glu Gln Gln Gly Tyr Asp His Leu Gln Gly Lys Arg	
205 210 215	
ata acc gaa aaa gaa gcg cgc aag att gcc caa aaa ttc gcc cag gac	1205
Ile Thr Glu Lys Glu Ala Arg Lys Ile Ala Gln Lys Phe Ala Gln Asp	
220 225 230 235	
aaa aat tac aat atc aaa gta tcg aaa agc ggc aag aaa acg aac agg	1253
Lys Asn Tyr Asn Ile Lys Val Ser Lys Ser Gly Lys Lys Thr Asn Arg	
240 245 250	
gat gta tac agc atc agt atg cag gac cct gat caa aaa gcg gat att	1301
Asp Val Tyr Ser Ile Ser Met Gln Asp Pro Asp Gln Lys Ala Asp Ile	
255 260 265	
tat atg gac att acc gaa aaa ggc gga tat ccg gtt tat ctg att caa	1349
Tyr Met Asp Ile Thr Glu Lys Gly Gly Tyr Pro Val Tyr Leu Ile Gln	
270 275 280	
aac aaa aaa att aaa gat gaa aaa atc agc tta aac gat gcg tca aac	1397
Asn Lys Lys Ile Lys Asp Glu Lys Ile Ser Leu Asn Asp Ala Ser Asn	
285 290 295	
aaa gcc ctt caa ttt ttg aaa aaa aac ggc tat aaa acg gaa gac ctg	1445
Lys Ala Leu Gln Phe Leu Lys Lys Asn Gly Tyr Lys Thr Glu Asp Leu	
300 305 310 315	
aag atg gat gaa agc tcg caa tac gac ggc gtc ggg gtg ttt tca ttt	1493
Lys Met Asp Glu Ser Ser Gln Tyr Asp Gly Val Gly Val Phe Ser Phe	
320 325 330	
gtt ccg gtc cag gac gat gtc tgg ctc tat ccg gac agc atc cgc atc	1541

Val	Pro	Val	Gln	Asp	Asp	Val	Trp	Leu	Tyr	Pro	Asp	Ser	Ile	Arg	Ile		
			335					340					345				
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Lys	Val	Ala	Leu	Asp	Asp	Gly	Glu	Ile	Thr	Gly	Phe	Asn	Ala	Lys	Asp		
		350					355					360					
ttc	tta	atc	tcc	cat	aaa	aaa	aga	gac	ttg	ccg	aag	ccc	aaa	cta	acg	1637	
Phe	Leu	Ile	Ser	His	Lys	Lys	Arg	Asp	Leu	Pro	Lys	Pro	Lys	Leu	Thr		
		365				370					375						
cct	gaa	aaa	gcg	aaa	gca	agc	ctg	aat	ccc	aac	gta	aaa	gtt	cag	gag	1685	
Pro	Glu	Lys	Ala	Lys	Ala	Ser	Leu	Asn	Pro	Asn	Val	Lys	Val	Gln	Glu		
380					385					390					395		
acg	cg	ctt	gct	tta	gtc	acg	aac	gag	ctt	tcg	caa	gaa	gtg	ctc	tgc	1733	
Thr	Arg	Leu	Ala	Leu	Val	Thr	Asn	Glu	Leu	Ser	Gln	Glu	Val	Leu	Cys		
			400					405					410				
tac	gaa	att	ctc	ggc	acg	att	gaa	aac	gat	aca	ttc	cg	atg	ttc	atc	1781	
Tyr	Glu	Ile	Leu	Gly	Thr	Ile	Glu	Asn	Asp	Thr	Phe	Arg	Met	Phe	Ile		
		415					420					425					
aat	gcc	aat	gac	ggc	acg	gaa	gag	aag	gtt	cag	aaa	atg	aaa	agc	gca	1829	
Asn	Ala	Asn	Asp	Gly	Thr	Glu	Glu	Lys	Val	Gln	Lys	Met	Lys	Ser	Ala		
		430					435				440						
gaa	ccg	ata	tac	aac	gac	ttg	taaaaaacgat	agatcaaagg	gaaaaggcga							1880	
Glu	Pro	Ile	Tyr	Asn	Asp	Leu											
		445			450												
taacatgcct	tttccttttt	agcattcgga	ataattcgcc	ctaaacattt	ccatactgaa											1940	
catatggg	cggaacgtccgc	cggtaaattg	aaaatgccc	gggccataaa	ttttccgggc											2000	
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cggtcatttt	aatcagcgtg	cagcttcttt	ttcattttctc	caaggctgag	ccttatctgt											2120	
caaagg	tcgt gcagtatgaa	ggcgtgaaca	acatgaaaat	cggcgaatgg	atcgagacat											2180	
ttaagccg	tta attcacgcta	aaatctcccc	tttttcgcct	aatacatgat	acaatcctat											2240	
aaggagtacc	agatagcaag	gagaggaatt	atggaaaaga	aattatgcat	tgcaatagac											2300	
ggccctgc	ggcagccggaaa	aagcaccgtg	gcgaaaatcg	tggccagaaa	aaa											2353	

<210> 119

<211> 450

<212> PRT

<213> Bacillus licheniformis

<400> 119

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20 25 30

Leu His Ala Glu Asn Asn Tyr Gln Arg Ala Phe His Asp Leu Thr Tyr  
35 40 45

Gln Val Asp Gln Leu His Asp Lys Ile Gly Ser Thr Leu Ala Met Asn  
50 55 60

Ser Lys Lys Thr Leu Ser Pro Ala Leu Ala Glu Val Trp Lys Thr Thr  
65 70 75 80

Ser Glu Ala His Asn Asn Val Ser Gln Leu Pro Leu Thr Leu Met Pro  
85 90 95

Phe Asn Lys Thr Glu Glu Phe Leu Ala Lys Val Gly Asp Phe Ser Tyr  
100 105 110

Lys Ala Ala Val Arg Asp Leu Asp Lys Glu Pro Leu Asn Lys Lys Glu  
115 120 125

Tyr Ala Ser Leu Asn Gln Leu Tyr Glu Asn Ser Lys Asp Ile Gln Asn  
130 135 140

Glu Leu Arg Asn Val Gln His Leu Ile Ile Asp Lys Asn Leu Arg Trp  
145 150 155 160

Met Asp Val Glu Leu Ala Leu Ala Ser Gly Gln Lys Gln Ser Asp Asn  
165 170 175

Lys Ile Ile Asn Gly Phe Lys Thr Val Glu Lys Ser Ala Ser Ala Phe  
180 185 190

Ser Asp Thr Asp Leu Gly Ala Thr Glu Met Thr Asn Thr Lys Lys Glu  
195 200 205

Gln Gln Gly Tyr Asp His Leu Gln Gly Lys Arg Ile Thr Glu Lys Glu  
210 215 220

Ala Arg Lys Ile Ala Gln Lys Phe Ala Gln Asp Lys Asn Tyr Asn Ile  
225 230 235 240

Lys Val Ser Lys Ser Gly Lys Lys Thr Asn Arg Asp Val Tyr Ser Ile  
245 250 255

Ser Met Gln Asp Pro Asp Gln Lys Ala Asp Ile Tyr Met Asp Ile Thr  
260 265 270

Glu Lys Gly Gly Tyr Pro Val Tyr Leu Ile Gln Asn Lys Lys Ile Lys  
275 280 285

Asp Glu Lys Ile Ser Leu Asn Asp Ala Ser Asn Lys Ala Leu Gln Phe  
290 295 300

Leu Lys Lys Asn Gly Tyr Lys Thr Glu Asp Leu Lys Met Asp Glu Ser  
305 310 315 320

Ser Gln Tyr Asp Gly Val Gly Val Phe Ser Phe Val Pro Val Gln Asp  
325 330 335

Asp Val Trp Leu Tyr Pro Asp Ser Ile Arg Ile Lys Val Ala Leu Asp  
340 345 350

Asp Gly Glu Ile Thr Gly Phe Asn Ala Lys Asp Phe Leu Ile Ser His  
355 360 365

Lys Lys Arg Asp Leu Pro Lys Pro Lys Leu Thr Pro Glu Lys Ala Lys  
370 375 380

Ala Ser Leu Asn Pro Asn Val Lys Val Gln Glu Thr Arg Leu Ala Leu  
385 390 395 400

Val Thr Asn Glu Leu Ser Gln Glu Val Leu Cys Tyr Glu Ile Leu Gly  
405 410 415

Thr Ile Glu Asn Asp Thr Phe Arg Met Phe Ile Asn Ala Asn Asp Gly  
420 425 430

Thr Glu Glu Lys Val Gln Lys Met Lys Ser Ala Glu Pro Ile Tyr Asn  
435 440 445

Asp Leu  
450



<210> 120  
 <211> 1355  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (249)..(1355)

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<400> 120
attccccctg atgtcatgat ggatcttccg agaattacga tgataggaag acttcacata      60

tatattgaaa accacagagg gcttttgctt ttcagcgata cggaagtaag gctgatgctc      120

aaacagggggc agtgcacatcat tcaaggcaaa gactttgtca tcaaaacgat tttgcctgag      180

gaaattctgc ttgaaggcac gattgagctt gtccgctata tcgattcata agtcgggggg      240

aaagaagc gtg aag aat aaa tgg ctt tct ttt ttt tca gga aag atc cag      290
      Val Lys Asn Lys Trp Leu Ser Phe Phe Ser Gly Lys Ile Gln
      1              5              10

ctt aag ata acg gga aaa ggg atc gaa cgg tta tta aat gaa tgc acc      338
Leu Lys Ile Thr Gly Lys Gly Ile Glu Arg Leu Leu Asn Glu Cys Thr
15              20              25              30

agg cgc aac atc ccg atg ttt aat gta aag aaa aag aaa gac gcc gtc      386
Arg Arg Asn Ile Pro Met Phe Asn Val Lys Lys Lys Lys Asp Ala Val
      35              40              45

ttt ctt tat att ccg ctt tct gat gta cat gcc ttc cgg aag gtc atc      434
Phe Leu Tyr Ile Pro Leu Ser Asp Val His Ala Phe Arg Lys Val Ile
      50              55              60

aga ggc ttc gac tgc aag tgc agg ttc atc aaa cga aaa ggg ttt cct      482
Arg Gly Phe Asp Cys Lys Cys Arg Phe Ile Lys Arg Lys Gly Phe Pro
      65              70              75

ttc ctc gtg cag aag tct aaa cgg aat agc ggc ttc act ttt gga gtt      530
Phe Leu Val Gln Lys Ser Lys Arg Asn Ser Gly Phe Thr Phe Gly Val
      80              85              90

gct gca ttt ttt atc atc atg ttc cta ttg tcc aac atg ctt tgg aaa      578
Ala Ala Phe Phe Ile Ile Met Phe Leu Leu Ser Asn Met Leu Trp Lys
95              100              105              110

att gat att aca gga gcc aat cca gag aca gaa cat caa atc aga cag      626
Ile Asp Ile Thr Gly Ala Asn Pro Glu Thr Glu His Gln Ile Arg Gln
      115              120              125

caa ttg gat caa atc ggc gtc aaa aaa ggc cgc ttt cag ttt tca atg      674
Gln Leu Asp Gln Ile Gly Val Lys Lys Gly Arg Phe Gln Phe Ser Met
      130              135              140

ctg acc ccg gaa aaa att cag cag gcg ctc aca aag cgg gtc gaa aac      722
Leu Thr Pro Glu Lys Ile Gln Gln Ala Leu Thr Lys Arg Val Glu Asn

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145	150	155	
atc act tgg gtg ggc att gag tta aac ggt acc gcc ctt cac atg aaa Ile Thr Trp Val Gly Ile Glu Leu Asn Gly Thr Ala Leu His Met Lys 160 165 170			770
gtc gtt gaa aag aat gaa cct gac aaa gaa aaa tat atc ggt ccg agg Val Val Glu Lys Asn Glu Pro Asp Lys Glu Lys Tyr Ile Gly Pro Arg 175 180 185 190			818
cac atc gtc gcc aaa aaa ggg gcg acc atc tcg aaa atg ttc gtg gaa His Ile Val Ala Lys Lys Gly Ala Thr Ile Ser Lys Met Phe Val Glu 195 200 205			866
aaa ggc gag ccg ctc gtc acg gtg aac cag cac gtt gaa aaa ggg caa Lys Gly Glu Pro Leu Val Thr Val Asn Gln His Val Glu Lys Gly Gln 210 215 220			914
atg ctc gtt tcc ggg ctg atc gga agc gaa gag gaa aag caa aaa gtc Met Leu Val Ser Gly Leu Ile Gly Ser Glu Glu Glu Lys Gln Lys Val 225 230 235			962
gga gca aaa ggg aaa atc tat ggt gaa acc tgg tac aag tca aca gta Gly Ala Lys Gly Lys Ile Tyr Gly Glu Thr Trp Tyr Lys Ser Thr Val 240 245 250			1010
acg gtt cct ctt gag aca tca ttt gac gtt ttt acg ggt aaa gta agg Thr Val Pro Leu Glu Thr Ser Phe Asp Val Phe Thr Gly Lys Val Arg 255 260 265 270			1058
aca agt cac aag cta tcc ctc gga tca tta acc atg ccg atc tgg ggc Thr Ser His Lys Leu Ser Leu Gly Ser Leu Thr Met Pro Ile Trp Gly 275 280 285			1106
ttt tca ttt aaa aaa gaa gac ttc tcg cgc ccg aag acg gag acc gaa Phe Ser Phe Lys Lys Glu Asp Phe Ser Arg Pro Lys Thr Glu Thr Glu 290 295 300			1154
aaa cac tcg ctg cat ttt ata aat ttt aag ctt cct gtc gct tat gaa Lys His Ser Leu His Phe Ile Asn Phe Lys Leu Pro Val Ala Tyr Glu 305 310 315			1202
aag gag cat atg agg gag agc gaa caa atc aaa agg gtg tac tcg aaa Lys Glu His Met Arg Glu Ser Glu Gln Ile Lys Arg Val Tyr Ser Lys 320 325 330			1250
aaa gaa gca gtt ctt aga agg aat cga aat ggg aaa aag aga cat cag Lys Glu Ala Val Leu Arg Arg Asn Arg Asn Gly Lys Lys Arg His Gln 335 340 345 350			1298
gac aaa aat cgg cag aga cgg gaa cat tat cag tgt aaa agt ttt gca Asp Lys Asn Arg Gln Arg Arg Glu His Tyr Gln Cys Lys Ser Phe Ala 355 360 365			1346
cac cac gag His His Glu			1355

<210> 121  
 <211> 369  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 121

Val Lys Asn Lys Trp Leu Ser Phe Phe Ser Gly Lys Ile Gln Leu Lys  
 1 5 10 15

Ile Thr Gly Lys Gly Ile Glu Arg Leu Leu Asn Glu Cys Thr Arg Arg  
 20 25 30

Asn Ile Pro Met Phe Asn Val Lys Lys Lys Lys Asp Ala Val Phe Leu  
 35 40 45

Tyr Ile Pro Leu Ser Asp Val His Ala Phe Arg Lys Val Ile Arg Gly  
 50 55 60

Phe Asp Cys Lys Cys Arg Phe Ile Lys Arg Lys Gly Phe Pro Phe Leu  
 65 70 75 80

Val Gln Lys Ser Lys Arg Asn Ser Gly Phe Thr Phe Gly Val Ala Ala  
 85 90 95

Phe Phe Ile Ile Met Phe Leu Leu Ser Asn Met Leu Trp Lys Ile Asp  
 100 105 110

Ile Thr Gly Ala Asn Pro Glu Thr Glu His Gln Ile Arg Gln Gln Leu  
 115 120 125

Asp Gln Ile Gly Val Lys Lys Gly Arg Phe Gln Phe Ser Met Leu Thr  
 130 135 140

Pro Glu Lys Ile Gln Gln Ala Leu Thr Lys Arg Val Glu Asn Ile Thr  
 145 150 155 160

Trp Val Gly Ile Glu Leu Asn Gly Thr Ala Leu His Met Lys Val Val  
 165 170 175

Glu Lys Asn Glu Pro Asp Lys Glu Lys Tyr Ile Gly Pro Arg His Ile  
 180 185 190

Val Ala Lys Lys Gly Ala Thr Ile Ser Lys Met Phe Val Glu Lys Gly  
 195 200 205

Glu Pro Leu Val Thr Val Asn Gln His Val Glu Lys Gly Gln Met Leu  
 210 215 220

Val Ser Gly Leu Ile Gly Ser Glu Glu Glu Lys Gln Lys Val Gly Ala  
 225 230 235 240

Lys Gly Lys Ile Tyr Gly Glu Thr Trp Tyr Lys Ser Thr Val Thr Val  
 245 250 255

Pro Leu Glu Thr Ser Phe Asp Val Phe Thr Gly Lys Val Arg Thr Ser  
 260 265 270

His Lys Leu Ser Leu Gly Ser Leu Thr Met Pro Ile Trp Gly Phe Ser  
 275 280 285

Phe Lys Lys Glu Asp Phe Ser Arg Pro Lys Thr Glu Thr Glu Lys His  
 290 295 300

Ser Leu His Phe Ile Asn Phe Lys Leu Pro Val Ala Tyr Glu Lys Glu  
 305 310 315 320

His Met Arg Glu Ser Glu Gln Ile Lys Arg Val Tyr Ser Lys Lys Glu  
 325 330 335

Ala Val Leu Arg Arg Asn Arg Asn Gly Lys Lys Arg His Gln Asp Lys  
 340 345 350

Asn Arg Gln Arg Arg Glu His Tyr Gln Cys Lys Ser Phe Ala His His  
 355 360 365

Glu

<210> 122  
 <211> 2120  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1625)

<400> 122  
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ttaccaagat ctcggcttaa aggcgacaaa gctgacaaag gaaaaagcaa tcgacgaagg 120  
cccgggctac acgagcattt ccttagaaaa gctgcctgat ttcgctggag attatatatt 180  
tataggacct tgggaatcaa gcggagacga cagcgccgtg cttaatacat ccatttggaa 240  
gaaccttggg gcggtcaaaa accaacaatgt ctataaaatc gaccctgtcg gcttctattt 300  
ttccgatccg atttcattag agggccagct cgaatttatt acagaaaact taacaaaata 360  
gaagaacttc cgcttgtca ggcggaagt ttttttgcgc gcgaaaccgg ggtgaaccct 420  
cattgaaaaa gcgattttca agtgcaagcc gggagagttt ttaaacgagc attcctcata 480  
tgctattgtg ggagggatca ttg atg gca ttc atc aac atc aaa ccg gag tta 533  
Leu Met Ala Phe Ile Asn Ile Lys Pro Glu Leu  
1 5 10  
aag cag aat atg gaa aga ctg tct gac att ctg aac ata ccc gaa ccg 581  
Lys Gln Asn Met Glu Arg Leu Ser Asp Ile Leu Asn Ile Pro Glu Pro  
15 20 25  
ctt tta atc agt gca aat gca aat gta tcc gcg gac gaa ctt tat ttt 629  
Leu Leu Ile Ser Ala Asn Ala Asn Val Ser Ala Asp Glu Leu Tyr Phe  
30 35 40  
ccg gga gta tct ttt cat gca gga aaa aac gtt caa gca gca gaa aca 677  
Pro Gly Val Ser Phe His Ala Gly Lys Asn Val Gln Ala Ala Glu Thr  
45 50 55  
tat gaa cag ctg caa tta ttg gcg aat caa tac acg ttt gaa gat gaa 725  
Tyr Glu Gln Leu Gln Leu Leu Ala Asn Gln Tyr Thr Phe Glu Asp Glu  
60 65 70 75  
cag tgg ctg aca aaa aca gcc gtt tac gat tca gca gaa ctg aaa aag 773  
Gln Trp Leu Thr Lys Thr Ala Val Tyr Asp Ser Ala Glu Leu Lys Lys  
80 85 90  
gaa att ggc aga ttg acg gaa tgc ttt ccg ttt gtt act tcc cgt atc 821  
Glu Ile Gly Arg Leu Thr Glu Cys Phe Pro Phe Val Thr Ser Arg Ile  
95 100 105  
atc ggc cgc tca agc atg ggc cag cct ata tat gaa ctg ctc ctt gga 869  
Ile Gly Arg Ser Ser Met Gly Gln Pro Ile Tyr Glu Leu Leu Leu Gly  
110 115 120  
gct gaa aat gcc gga aaa aga acg cat atg aat gcc tct ttt cat gcc 917  
Ala Glu Asn Ala Gly Lys Arg Thr His Met Asn Ala Ser Phe His Ala  
125 130 135  
aat gaa tgg atc acc act tct gtt ttg atg aaa tgg ctc aaa gaa tac 965  
Asn Glu Trp Ile Thr Thr Ser Val Leu Met Lys Trp Leu Lys Glu Tyr  
140 145 150 155

tgt tat cat tta tgt aca ggc cag acc gct tta ggt ttt tcg ccg ctc	1013
Cys Tyr His Leu Cys Thr Gly Gln Thr Ala Leu Gly Phe Ser Pro Leu	
160 165 170	
gat att ttt tca tca aca aag ctt tcc gtc gtg ccg atc gtt aat ccc	1061
Asp Ile Phe Ser Ser Thr Lys Leu Ser Val Val Pro Ile Val Asn Pro	
175 180 185	
gac ggt gtt gac ctt gta ctt aac ggc ccc ggt cat ctt ggg atc gcg	1109
Asp Gly Val Asp Leu Val Leu Asn Gly Pro Gly His Leu Gly Ile Ala	
190 195 200	
aga gaa gcg ctg gat gag atg aac gag cat cag ccg gat ttc ccg gaa	1157
Arg Glu Ala Leu Asp Glu Met Asn Glu His Gln Pro Asp Phe Arg Glu	
205 210 215	
tgg aaa gcc aat ata aac gga gtg gat tta aat aat cag ttt ccg tct	1205
Trp Lys Ala Asn Ile Asn Gly Val Asp Leu Asn Asn Gln Phe Pro Ser	
220 225 230 235	
ttc tgg gag atc gaa aaa caa aga aaa ccg cct aaa tcc cct tcc tac	1253
Phe Trp Glu Ile Glu Lys Gln Arg Lys Pro Pro Lys Ser Pro Ser Tyr	
240 245 250	
aga gac tac ccc gga gat gaa ccg ctg aca gaa ccg gaa gcg gca gcg	1301
Arg Asp Tyr Pro Gly Asp Glu Pro Leu Thr Glu Pro Glu Ala Ala Ala	
255 260 265	
atg agg gat tta atc gca aac gag ccg cct gac cgg ctt gtg gcg ctt	1349
Met Arg Asp Leu Ile Ala Asn Glu Pro Pro Asp Arg Leu Val Ala Leu	
270 275 280	
cac aca cag ggg gag gaa att tat tgg gga tac aag gga ttg gag cct	1397
His Thr Gln Gly Glu Glu Ile Tyr Trp Gly Tyr Lys Gly Leu Glu Pro	
285 290 295	
cct gaa tca gct gat gtg atc caa aca ttt gag cgc ctg agc ggt tat	1445
Pro Glu Ser Ala Asp Val Ile Gln Thr Phe Glu Arg Leu Ser Gly Tyr	
300 305 310 315	
aag ggc gtc aga tat ata gac agc tat gca gga ttt aga gat tgg ttt	1493
Lys Gly Val Arg Tyr Ile Asp Ser Tyr Ala Gly Phe Arg Asp Trp Phe	
320 325 330	
att cat tat tac gga aga gaa gga tat act gtt gaa ctt ggc aaa gga	1541
Ile His Tyr Tyr Gly Arg Glu Gly Tyr Thr Val Glu Leu Gly Lys Gly	
335 340 345	
aaa aat cct tta ccg ctg aaa caa ttt gac gat ata tat tgt aaa agc	1589
Lys Asn Pro Leu Pro Leu Lys Gln Phe Asp Asp Ile Tyr Cys Lys Ser	
350 355 360	
aga gga ata ctt tgg gca tcc tgt ttt ttt gaa agc tgaaactttt	1635
Arg Gly Ile Leu Trp Ala Ser Cys Phe Phe Glu Ser	
365 370 375	

cacggtgaaa atcgtaaatt agacagccaa acatttatgg agggagaatg gccggtttga 1695  
 gagtttcatt attgattatt gccgctctga tggccgtggc tgcggctggt tgcacgccgc 1755  
 agcatcaaga aggatcaaaa agcgttcatc atgaggagcc ggaagggaaa agagaaagcg 1815  
 gtgcagcagt aaaagataaa aaagtgatag cgctgaagga ccggcacttt gatgagacgg 1875  
 caggatggct tgataatgaa accgttatat acaccgcaac cgatccggtc ggaggaagtg 1935  
 aaatcaaadc atatgatata tttaaaggga cgggcaaaac gatctacaag acagatgaca 1995  
 ggctgatagc gtcggaagtc aacagtgaaa aaggcatgat tcttatccaa accgccggaa 2055  
 acggctctga aatgaagtta actttgctta atttacaggg gaaacagctg tttgcaaaaa 2115  
 aattt 2120

<210> 123  
 <211> 375  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 123

Leu Met Ala Phe Ile Asn Ile Lys Pro Glu Leu Lys Gln Asn Met Glu  
 1 5 10 15

Arg Leu Ser Asp Ile Leu Asn Ile Pro Glu Pro Leu Leu Ile Ser Ala  
 20 25 30

Asn Ala Asn Val Ser Ala Asp Glu Leu Tyr Phe Pro Gly Val Ser Phe  
 35 40 45

His Ala Gly Lys Asn Val Gln Ala Ala Glu Thr Tyr Glu Gln Leu Gln  
 50 55 60

Leu Leu Ala Asn Gln Tyr Thr Phe Glu Asp Glu Gln Trp Leu Thr Lys  
 65 70 75 80

Thr Ala Val Tyr Asp Ser Ala Glu Leu Lys Lys Glu Ile Gly Arg Leu  
 85 90 95

Thr Glu Cys Phe Pro Phe Val Thr Ser Arg Ile Ile Gly Arg Ser Ser  
 100 105 110

Met Gly Gln Pro Ile Tyr Glu Leu Leu Leu Gly Ala Glu Asn Ala Gly  
 115 120 125

Lys Arg Thr His Met Asn Ala Ser Phe His Ala Asn Glu Trp Ile Thr  
 130 135 140

Thr Ser Val Leu Met Lys Trp Leu Lys Glu Tyr Cys Tyr His Leu Cys  
 145 150 155 160

Thr Gly Gln Thr Ala Leu Gly Phe Ser Pro Leu Asp Ile Phe Ser Ser  
 165 170 175

Thr Lys Leu Ser Val Val Pro Ile Val Asn Pro Asp Gly Val Asp Leu  
 180 185 190

Val Leu Asn Gly Pro Gly His Leu Gly Ile Ala Arg Glu Ala Leu Asp  
 195 200 205

Glu Met Asn Glu His Gln Pro Asp Phe Arg Glu Trp Lys Ala Asn Ile  
 210 215 220

Asn Gly Val Asp Leu Asn Asn Gln Phe Pro Ser Phe Trp Glu Ile Glu  
 225 230 235 240

Lys Gln Arg Lys Pro Pro Lys Ser Pro Ser Tyr Arg Asp Tyr Pro Gly  
 245 250 255

Asp Glu Pro Leu Thr Glu Pro Glu Ala Ala Ala Met Arg Asp Leu Ile  
 260 265 270

Ala Asn Glu Pro Pro Asp Arg Leu Val Ala Leu His Thr Gln Gly Glu  
 275 280 285

Glu Ile Tyr Trp Gly Tyr Lys Gly Leu Glu Pro Pro Glu Ser Ala Asp  
 290 295 300

Val Ile Gln Thr Phe Glu Arg Leu Ser Gly Tyr Lys Gly Val Arg Tyr  
 305 310 315 320

Ile Asp Ser Tyr Ala Gly Phe Arg Asp Trp Phe Ile His Tyr Tyr Gly  
 325 330 335

Arg Glu Gly Tyr Thr Val Glu Leu Gly Lys Gly Lys Asn Pro Leu Pro  
 340 345 350



Leu Lys Gln Phe Asp Asp Ile Tyr Cys Lys Ser Arg Gly Ile Leu Trp  
 355 360 365

Ala Ser Cys Phe Phe Glu Ser  
 370 375

<210> 124  
 <211> 1597  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (342)..(1094)

<400> 124  
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 aaagcgatgg tcatctcaaa actgtaacca attattttct tgatagtgtg gctgcgacta 120  
 ttatgcgctg attgtttacg gtgcttgctt tttataccat tggttcattt gaccggaatc 180  
 gtgttttgat tgcaggaatt tttgttactg tttgtgaaaa aacagcagaa gaaaaacagc 240  
 ggaaaaactcg cgtcttaggg cggatttcca aaaaaatgtc gtaaattcga tgcataaatt 300  
 tgatgaaatc gcccggccat gcggtataat agattttgtg a atg aaa gat tca atg 356  
 Met Lys Asp Ser Met  
 1 5  
 ttg aaa gag agt ggt tac atc atg ggc cgt aaa tgg aac aat ata aaa 404  
 Leu Lys Glu Ser Gly Tyr Ile Met Gly Arg Lys Trp Asn Asn Ile Lys  
 10 15 20  
 gag aag aaa gcg tcc aag gat gcg aat acg agc cga atc tac gcg aag 452  
 Glu Lys Lys Ala Ser Lys Asp Ala Asn Thr Ser Arg Ile Tyr Ala Lys  
 25 30 35  
 ttc ggc cgc gaa atc tat gtg gcg gca aag cag gga gag ccc gat ccc 500  
 Phe Gly Arg Glu Ile Tyr Val Ala Ala Lys Gln Gly Glu Pro Asp Pro  
 40 45 50  
 gaa ctg aac cag aac ctg aaa ttc gtg ctt gag cgc gcc aaa aca tac 548  
 Glu Leu Asn Gln Asn Leu Lys Phe Val Leu Glu Arg Ala Lys Thr Tyr  
 55 60 65  
 aat gtc ccg aaa gcg att att gag cgg gcg atc gaa aaa gcg aag ggc 596  
 Asn Val Pro Lys Ala Ile Ile Glu Arg Ala Ile Glu Lys Ala Lys Gly  
 70 75 80 85  
 ggc tct gag gaa aat tac gac gag ctg cgc tat gaa ggc ttc ggt ccg 644  
 Gly Ser Glu Glu Asn Tyr Asp Glu Leu Arg Tyr Glu Gly Phe Gly Pro  
 90 95 100

aac gga gcg atg gtg atc gtt gac gcg ttg aca aac aac gtc aac cgc	692
Asn Gly Ala Met Val Ile Val Asp Ala Leu Thr Asn Asn Val Asn Arg	
105 110 115	
acg gct gcc gat gtg cgc tcc aca ttt ggc aaa aac ggc gga aac atg	740
Thr Ala Ala Asp Val Arg Ser Thr Phe Gly Lys Asn Gly Gly Asn Met	
120 125 130	
gga gtg agc gga tct gtc gct tac atg ttt gat ccg acg gcc gtc atc	788
Gly Val Ser Gly Ser Val Ala Tyr Met Phe Asp Pro Thr Ala Val Ile	
135 140 145	
ggc ttt gaa ggc aaa acg gct gat gaa acg ctc gaa tta ttg atg gaa	836
Gly Phe Glu Gly Lys Thr Ala Asp Glu Thr Leu Glu Leu Leu Met Glu	
150 155 160 165	
gcg gat atc gat gtc cgt gat att tta gag gaa gac gat gca gtg atc	884
Ala Asp Ile Asp Val Arg Asp Ile Leu Glu Glu Asp Asp Ala Val Ile	
170 175 180	
gtc tat gcc gag ccc gat cag ttc cac gcc gta cag gag gcg ctg caa	932
Val Tyr Ala Glu Pro Asp Gln Phe His Ala Val Gln Glu Ala Leu Gln	
185 190 195	
aac gcc ggc att act gag ttc acg gtg gcc gag ctg acg atg ctc gcg	980
Asn Ala Gly Ile Thr Glu Phe Thr Val Ala Glu Leu Thr Met Leu Ala	
200 205 210	
caa aat gac gtc gcc ctt cca gag gac gcg cgc gca cag ttt gaa aag	1028
Gln Asn Asp Val Ala Leu Pro Glu Asp Ala Arg Ala Gln Phe Glu Lys	
215 220 225	
ctg att gac gcg ctg gaa gat ctg gaa gac gtt cag caa gtt tac cat	1076
Leu Ile Asp Ala Leu Glu Asp Leu Glu Asp Val Gln Gln Val Tyr His	
230 235 240 245	
aat gtc gat tta ggg gcg taaaaagagg ccctgaaaaa atcgggaaaag	1124
Asn Val Asp Leu Gly Ala	
250	
aaaagataga tgaacaggag gacgacctgt tttgtctatc ttttttttatt gtaaagttaa	1184
cttgacattt tatttttttg ttaagtatac tttagctata gtgaacttta cattcccaat	1244
ggaggaaaaga tgaaaacgtt aataaaggaa aagcgcactt cgctgaacat gacacaagaa	1304
gaactggcta aaaggcttaa tgtgtcgagg caaacggtga tttcccttga aaagggaaaa	1364
tataaacctt cactcgttct ggcgcataaa ctgggtcaaa tttttgaatg tctgattgaa	1424
gatttattta tttttgaggg ggatgaaaat attgactgaa acgatgacaa acatactgat	1484
cgcttttagcg ggcttagaat aggcgtgctc gggatcgcaa ttgtttacaa agtaaacaga	1544
cgaattggaa aaaaagagag gctgttcgat gagcgccagc agaagattag cta	1597

<210> 125  
 <211> 251  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 125

Met Lys Asp Ser Met Leu Lys Glu Ser Gly Tyr Ile Met Gly Arg Lys  
 1 5 10 15

Trp Asn Asn Ile Lys Glu Lys Lys Ala Ser Lys Asp Ala Asn Thr Ser  
 20 25 30

Arg Ile Tyr Ala Lys Phe Gly Arg Glu Ile Tyr Val Ala Ala Lys Gln  
 35 40 45

Gly Glu Pro Asp Pro Glu Leu Asn Gln Asn Leu Lys Phe Val Leu Glu  
 50 55 60

Arg Ala Lys Thr Tyr Asn Val Pro Lys Ala Ile Ile Glu Arg Ala Ile  
 65 70 75 80

Glu Lys Ala Lys Gly Gly Ser Glu Glu Asn Tyr Asp Glu Leu Arg Tyr  
 85 90 95

Glu Gly Phe Gly Pro Asn Gly Ala Met Val Ile Val Asp Ala Leu Thr  
 100 105 110

Asn Asn Val Asn Arg Thr Ala Ala Asp Val Arg Ser Thr Phe Gly Lys  
 115 120 125

Asn Gly Gly Asn Met Gly Val Ser Gly Ser Val Ala Tyr Met Phe Asp  
 130 135 140

Pro Thr Ala Val Ile Gly Phe Glu Gly Lys Thr Ala Asp Glu Thr Leu  
 145 150 155 160

Glu Leu Leu Met Glu Ala Asp Ile Asp Val Arg Asp Ile Leu Glu Glu  
 165 170 175

Asp Asp Ala Val Ile Val Tyr Ala Glu Pro Asp Gln Phe His Ala Val  
 180 185 190

Gln Glu Ala Leu Gln Asn Ala Gly Ile Thr Glu Phe Thr Val Ala Glu  
 195 200 205

Leu Thr Met Leu Ala Gln Asn Asp Val Ala Leu Pro Glu Asp Ala Arg  
 210 215 220

Ala Gln Phe Glu Lys Leu Ile Asp Ala Leu Glu Asp Leu Glu Asp Val  
 225 230 235 240

Gln Gln Val Tyr His Asn Val Asp Leu Gly Ala  
 245 250

<210> 126  
 <211> 1888  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (3)..(1385)

<400> 126  
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 Lys Asp Ala Ala Arg Arg Asn Val Asp Asp Ala Arg Thr Gly Ile  
 1 5 10 15

att gct ttc tcc att cta tat ttg tcc gcc ccg ttt ttt gca gag atg 95  
 Ile Ala Phe Ser Ile Leu Tyr Leu Ser Ala Pro Phe Phe Ala Glu Met  
 20 25 30

gcc ctt ggc gga aca gaa aac aac ggg ctg acg ctt gaa cat gtc gtg 143  
 Ala Leu Gly Gly Thr Glu Asn Asn Gly Leu Thr Leu Glu His Val Val  
 35 40 45

tat gtc att cgc atg gtc agt ctc gcg cta ctg gtt gtg ccg atc ttg 191  
 Tyr Val Ile Arg Met Val Ser Leu Ala Leu Leu Val Val Pro Ile Leu  
 50 55 60

gcg ctg atc aga ggc ttt ttc caa ggt cac cag atg atg ggg ccg aca 239  
 Ala Leu Ile Arg Gly Phe Phe Gln Gly His Gln Met Met Gly Pro Thr  
 65 70 75

gcc gtt tca cag gta gtt gaa caa att gcc aga atc gtc ttt cta tta 287  
 Ala Val Ser Gln Val Val Glu Gln Ile Ala Arg Ile Val Phe Leu Leu  
 80 85 90 95

acg gcc act tac ttg gtg atc aaa gta tta aac ggc ggg ctt gtc gtc 335  
 Thr Ala Thr Tyr Leu Val Ile Lys Val Leu Asn Gly Gly Leu Val Val  
 100 105 110

gct gtc ggc tat gcg act ttt gcg gct ttg atc gga gcg ttc gcc gga 383  
 Ala Val Gly Tyr Ala Thr Phe Ala Ala Leu Ile Gly Ala Phe Ala Gly  
 115 120 125

ctg ttc act ctt tac ttt tcc tgg cag aaa aga aaa ggg gcg ctc ctg	431
Leu Phe Thr Leu Tyr Phe Ser Trp Gln Lys Arg Lys Gly Ala Leu Leu	
130 135 140	
gcg ctg aag ccg aac ctt gtt cct tca gcc gat att acg tac cgg caa	479
Ala Leu Lys Pro Asn Leu Val Pro Ser Ala Asp Ile Thr Tyr Arg Gln	
145 150 155	
atg ttt aaa gag ctg ttc agc tat gcc gcc cct tat gtc ttt gtc ggg	527
Met Phe Lys Glu Leu Phe Ser Tyr Ala Ala Pro Tyr Val Phe Val Gly	
160 165 170 175	
ctg gcg ata ccg ctt tac cag tac att gat acg aat acg ttt aat aaa	575
Leu Ala Ile Pro Leu Tyr Gln Tyr Ile Asp Thr Asn Thr Phe Asn Lys	
180 185 190	
gcg atg att gca gcc ggc tat caa aac atc agc cag gat ttg atg gcg	623
Ala Met Ile Ala Ala Gly Tyr Gln Asn Ile Ser Gln Asp Leu Met Ala	
195 200 205	
atc gtg acg ctg tac gtg cca aag ctt gtg atg att ccg gta tct ctc	671
Ile Val Thr Leu Tyr Val Pro Lys Leu Val Met Ile Pro Val Ser Leu	
210 215 220	
gcg acg gca ttc ggg ctg aca ttg att ccg gcg gtg act gaa aac ttt	719
Ala Thr Ala Phe Gly Leu Thr Leu Ile Pro Ala Val Thr Glu Asn Phe	
225 230 235	
acc aac aaa gat ttc cct gct tta aac aaa cag att gat cag gcg atg	767
Thr Asn Lys Asp Phe Pro Ala Leu Asn Lys Gln Ile Asp Gln Ala Met	
240 245 250 255	
cag atc att ctc ttc atc gtt ctt ccg gca tca gtc ggt atg gct ctt	815
Gln Ile Ile Leu Phe Ile Val Leu Pro Ala Ser Val Gly Met Ala Leu	
260 265 270	
ttg tcg ggg ccg gtt tac acg ttc ttt tac ggc tcg gaa agc ctg ctc	863
Leu Ser Gly Pro Val Tyr Thr Phe Phe Tyr Gly Ser Glu Ser Leu Leu	
275 280 285	
cct gac atg gga cga gat att ttg ttc tgg tac gcg cct gtg gcg ctg	911
Pro Asp Met Gly Arg Asp Ile Leu Phe Trp Tyr Ala Pro Val Ala Leu	
290 295 300	
tta ttc tcg ctc ttc acc gtc aac gct gca att ttg cag ggg gtg aac	959
Leu Phe Ser Leu Phe Thr Val Asn Ala Ala Ile Leu Gln Gly Val Asn	
305 310 315	
aag cag aaa ttt gcg gtt gtc agc ttg atg atc ggg att gtg atc aaa	1007
Lys Gln Lys Phe Ala Val Val Ser Leu Met Ile Gly Ile Val Ile Lys	
320 325 330 335	
atc gcg ctt aac gtt ccg ctc atc aag ctg ctt caa ggc agc ggg tcg	1055
Ile Ala Leu Asn Val Pro Leu Ile Lys Leu Leu Gln Gly Ser Gly Ser	
340 345 350	
att ttg gca acg gcg ctc ggc tat tca gct tca ctc cta tac gga ttt	1103

Ile	Leu	Ala	Thr	Ala	Leu	Gly	Tyr	Ser	Ala	Ser	Leu	Leu	Tyr	Gly	Phe		
			355					360					365				
atc	atg	att	aaa	cgc	cat	gcc	ggc	tat	tcg	tat	cgc	aaa	ctg	ttt	aaa	1151	
Ile	Met	Ile	Lys	Arg	His	Ala	Gly	Tyr	Ser	Tyr	Arg	Lys	Leu	Phe	Lys		
		370					375					380					
cgg	ttt	ttg	ctg	atg	ctg	atc	ctg	acg	gcg	gtc	atg	ggc	atc	att	ttg	1199	
Arg	Phe	Leu	Leu	Met	Leu	Ile	Leu	Thr	Ala	Val	Met	Gly	Ile	Ile	Leu		
		385				390					395						
ctg	ctt	gtc	cag	gcg	ctt	cta	agt	att	ttt	att	tca	tac	gaa	ggc	ggg	1247	
Leu	Leu	Val	Gln	Ala	Leu	Leu	Ser	Ile	Phe	Ile	Ser	Tyr	Glu	Gly	Gly		
400					405					410					415		
cag	atc	agg	tct	gct	gtc	gtc	att	ttc	atc	aca	acc	gca	gtg	ggc	ggg	1295	
Gln	Ile	Arg	Ser	Ala	Val	Val	Ile	Phe	Ile	Thr	Thr	Ala	Val	Gly	Gly		
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tca	gtt	tat	ctg	tac	ttg	gct	tac	cgt	gtg	aaa	ctg	ctc	gaa	aaa	atc	1343	
Ser	Val	Tyr	Leu	Tyr	Leu	Ala	Tyr	Arg	Val	Lys	Leu	Leu	Glu	Lys	Ile		
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ttc	ggt	cag	cga	ttg	aat	cgc	ttt	ttc	aaa	aga	aag	gcc	tcc			1385	
Phe	Gly	Gln	Arg	Leu	Asn	Arg	Phe	Phe	Lys	Arg	Lys	Ala	Ser				
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taaaaagggc	ttttcttttt	atgtaaaaaa	aggggtgtct	tcatgagatt	ggataaaactg											1445	
ttgtcaaaca	gcggttatgg	ttcgagaaaa	gaagtcaaaa	aaatgctgaa	aaacggcgcg											1505	
gtgcgcgtca	atgatcaatt	agtcaaagac	gccaaaaagc	acgttgaccc	ggaatcagac											1565	
gacatcacgg	tatacggggc	accggtcatg	taccgggaat	ttatttactt	aatgatgaac											1625	
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 <212> PRT  
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 <400> 127

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Ala Phe Ser Ile Leu Tyr Leu Ser Ala Pro Phe Phe Ala Glu Met Ala  
20 25 30

Leu Gly Gly Thr Glu Asn Asn Gly Leu Thr Leu Glu His Val Val Tyr  
35 40 45

Val Ile Arg Met Val Ser Leu Ala Leu Leu Val Val Pro Ile Leu Ala  
50 55 60

Leu Ile Arg Gly Phe Phe Gln Gly His Gln Met Met Gly Pro Thr Ala  
65 70 75 80

Val Ser Gln Val Val Glu Gln Ile Ala Arg Ile Val Phe Leu Leu Thr  
85 90 95

Ala Thr Tyr Leu Val Ile Lys Val Leu Asn Gly Gly Leu Val Val Ala  
100 105 110

Val Gly Tyr Ala Thr Phe Ala Ala Leu Ile Gly Ala Phe Ala Gly Leu  
115 120 125

Phe Thr Leu Tyr Phe Ser Trp Gln Lys Arg Lys Gly Ala Leu Leu Ala  
130 135 140

Leu Lys Pro Asn Leu Val Pro Ser Ala Asp Ile Thr Tyr Arg Gln Met  
145 150 155 160

Phe Lys Glu Leu Phe Ser Tyr Ala Ala Pro Tyr Val Phe Val Gly Leu  
165 170 175

Ala Ile Pro Leu Tyr Gln Tyr Ile Asp Thr Asn Thr Phe Asn Lys Ala  
180 185 190

Met Ile Ala Ala Gly Tyr Gln Asn Ile Ser Gln Asp Leu Met Ala Ile  
195 200 205

Val Thr Leu Tyr Val Pro Lys Leu Val Met Ile Pro Val Ser Leu Ala  
210 215 220

Thr Ala Phe Gly Leu Thr Leu Ile Pro Ala Val Thr Glu Asn Phe Thr  
225 230 235 240

Asn Lys Asp Phe Pro Ala Leu Asn Lys Gln Ile Asp Gln Ala Met Gln

245										250										255														
Ile	Ile	Leu	Phe	Ile	Val	Leu	Pro	Ala	Ser	Val	Gly	Met	Ala	Leu	Leu																			
			260						265					270																				
Ser	Gly	Pro	Val	Tyr	Thr	Phe	Phe	Tyr	Gly	Ser	Glu	Ser	Leu	Leu	Pro																			
		275					280					285																						
Asp	Met	Gly	Arg	Asp	Ile	Leu	Phe	Trp	Tyr	Ala	Pro	Val	Ala	Leu	Leu																			
	290					295					300																							
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305					310					315					320																			
Gln	Lys	Phe	Ala	Val	Val	Ser	Leu	Met	Ile	Gly	Ile	Val	Ile	Lys	Ile																			
				325					330					335																				
Ala	Leu	Asn	Val	Pro	Leu	Ile	Lys	Leu	Leu	Gln	Gly	Ser	Gly	Ser	Ile																			
		340					345					350																						
Leu	Ala	Thr	Ala	Leu	Gly	Tyr	Ser	Ala	Ser	Leu	Leu	Tyr	Gly	Phe	Ile																			
		355					360					365																						
Met	Ile	Lys	Arg	His	Ala	Gly	Tyr	Ser	Tyr	Arg	Lys	Leu	Phe	Lys	Arg																			
	370					375					380																							
Phe	Leu	Leu	Met	Leu	Ile	Leu	Thr	Ala	Val	Met	Gly	Ile	Ile	Leu	Leu																			
385					390					395				400																				
Leu	Val	Gln	Ala	Leu	Leu	Ser	Ile	Phe	Ile	Ser	Tyr	Glu	Gly	Gly	Gln																			
			405					410					415																					
Ile	Arg	Ser	Ala	Val	Val	Ile	Phe	Ile	Thr	Thr	Ala	Val	Gly	Gly	Ser																			
		420					425					430																						
Val	Tyr	Leu	Tyr	Leu	Ala	Tyr	Arg	Val	Lys	Leu	Leu	Glu	Lys	Ile	Phe																			
	435					440						445																						
Gly	Gln	Arg	Leu	Asn	Arg	Phe	Phe	Lys	Arg	Lys	Ala	Ser																						
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<210> 128  
 <211> 1852



<213> Bacillus licheniformis

<221> CDS

<222> (501) . . (1349)

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acgcgcctgtc gccgccttt cggttctcag cgaqctctgc cttccgcttg tgaaaaaaga 180

cqgtttattc qtagcattaa aaqccqcttc qqctgatgaa gaaattgaaa cgggcaaaaa 240

agccatcaaa acgcttqqag qcaaaattqa aaccgtacat tcttttcagc tgccaataga 300

agaaagcgaa agaaacatca ttgtcatcaa aaaacaatcg cagacaccga agaaatttcc 360

aagaaaqcct ggaacaccta ataaatctcc tattgaaggt taaattattc gttttcttca 420

aatttcgtga tgtcacagaa qgaaaattca tqagaaaata gaattataaa aatggcagtg 480

tttaaagggtg gtgtaggtac atg aag cat tca ttc tct cgt ctc ttc gga ctt 533  
Met Lys His Ser Phe Ser Arg Leu Phe Gly Leu  
1 5 10

ggc gac aag gaa gaa gaa gca gag att gct gaa cat gat acg aat aaa 581  
Gly Asp Lys Glu Glu Glu Ala Glu Ile Ala Glu His Asp Thr Asn Lys  
15 20 25

gaa gaa att caa gag att cca gta ggc gat ata att cct aac cgt ttt 629  
Glu Glu Ile Gln Glu Ile Pro Val Gly Asp Ile Ile Pro Asn Arg Phe  
30 35 40

cag ccg cgc acc att ttc tca gaa gaa aaa att aaa gaa tta gct gca 677  
Gln Pro Arg Thr Ile Phe Ser Glu Glu Lys Ile Lys Glu Leu Ala Ala  
45 50 55

acc att cat aca cac ggc att atc cag ccg att gtc gtc aga aaa aca 725  
Thr Ile His Thr His Gly Ile Ile Gln Pro Ile Val Val Arg Lys Thr  
60 65 70 75

gag cgg gaa ggc caa tat gaa ctc ata gcc gga gag cgg cgc tgg cgg 773  
Glu Arg Glu Gly Gln Tyr Glu Leu Ile Ala Gly Glu Arg Arg Trp Arg  
80 85 90

gcg gtt caa acg ctc gat tgg gag aag gtt ccc gct att att aag gat 821  
Ala Val Gln Thr Leu Asp Trp Glu Lys Val Pro Ala Ile Ile Lys Asp  
95 100 105

ttt tca gat aca gag acc gct tct gtc gct ctt atc gaa aac ctt cag 869  
Phe Ser Asp Thr Glu Thr Ala Ser Val Ala Leu Ile Glu Asn Leu Gln  
110 115 120

agg gaa gaa tta tct tcg att gaa gag gcg cat gct tat gca agg ctt	917
Arg Glu Glu Leu Ser Ser Ile Glu Glu Ala His Ala Tyr Ala Arg Leu	
125 130 135	
tta gag ctt cac gat ttg acg cag gaa gcc ctt gca caa agg ctt gga	965
Leu Glu Leu His Asp Leu Thr Gln Glu Ala Leu Ala Gln Arg Leu Gly	
140 145 150 155	
aag ggc cag tca aca atc gcc aat aag ctc aga ctg tta aag ctt ccg	1013
Lys Gly Gln Ser Thr Ile Ala Asn Lys Leu Arg Leu Leu Lys Leu Pro	
160 165 170	
gaa gag gtg cag gaa gcg atc ttg aaa aaa gaa att tca gag cgc cac	1061
Glu Glu Val Gln Glu Ala Ile Leu Lys Lys Glu Ile Ser Glu Arg His	
175 180 185	
gca aga gcg ctc ata ccg ttg aaa cag ccc gac ctt cag gtc aag ctg	1109
Ala Arg Ala Leu Ile Pro Leu Lys Gln Pro Asp Leu Gln Val Lys Leu	
190 195 200	
ctg cat gaa gtc att gaa aag agt tta aat gta aaa caa acc gaa gac	1157
Leu His Glu Val Ile Glu Lys Ser Leu Asn Val Lys Gln Thr Glu Asp	
205 210 215	
cgt gtc gtc aaa atg ctt gag cag gat aaa cgc aag cct aaa cca aag	1205
Arg Val Val Lys Met Leu Glu Gln Asp Lys Arg Lys Pro Lys Pro Lys	
220 225 230 235	
aga aaa gcg tac agc agg gac gcg aga atc gcg atg aat acg att cgc	1253
Arg Lys Ala Tyr Ser Arg Asp Ala Arg Ile Ala Met Asn Thr Ile Arg	
240 245 250	
cag tcc tta tca atg gtg gaa gac agc ggc gtc aaa ctg aat acg gaa	1301
Gln Ser Leu Ser Met Val Glu Asp Ser Gly Val Lys Leu Asn Thr Glu	
255 260 265	
gaa gag gaa ttt gaa gaa tat att cag ttt acg att cga ata ccg aaa	1349
Glu Glu Glu Phe Glu Glu Tyr Ile Gln Phe Thr Ile Arg Ile Pro Lys	
270 275 280	
taaaagctcc ctatagagct tttatTTTTT taggcaaaat atctatgggg gagcgtctat	1409
ggaatattat cgacaatatc attcattgct tttttcgatt gcttaccgta tgctcgggtc	1469
ttttcaagat gcagaggaca tcatccaaga attgttcgca gaccttcagg aaaaagatat	1529
cggTcaaatt gaccatattc aagcatatTT aacgaaatca atcacaaacc gctgcataaa	1589
tgaactgcag tctgcccgcga agaagcggga ggtatatatc ggggaatggc ttccggaacc	1649
gcaggTggcg ctttcagctc aaatcccggc tgagtacgtt gaagagaaag aaaaggTatc	1709
ctatgctttt ctggtagtta tgagccgatt aaatcctgta gaaagagccg ttttgatgtt	1769
tagagaagta tttggatatc attacaagga aatttcgtcc attatcggga agtcggaagc	1829
gaactgtcgt caaatccaca gcc	1852

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 <212> PRT  
 <213> Bacillus licheniformis

<400> 129

Met Lys His Ser Phe Ser Arg Leu Phe Gly Leu Gly Asp Lys Glu Glu  
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Glu Ala Glu Ile Ala Glu His Asp Thr Asn Lys Glu Glu Ile Gln Glu  
 20 25 30

Ile Pro Val Gly Asp Ile Ile Pro Asn Arg Phe Gln Pro Arg Thr Ile  
 35 40 45

Phe Ser Glu Glu Lys Ile Lys Glu Leu Ala Ala Thr Ile His Thr His  
 50 55 60

Gly Ile Ile Gln Pro Ile Val Val Arg Lys Thr Glu Arg Glu Gly Gln  
 65 70 75 80

Tyr Glu Leu Ile Ala Gly Glu Arg Arg Trp Arg Ala Val Gln Thr Leu  
 85 90 95

Asp Trp Glu Lys Val Pro Ala Ile Ile Lys Asp Phe Ser Asp Thr Glu  
 100 105 110

Thr Ala Ser Val Ala Leu Ile Glu Asn Leu Gln Arg Glu Glu Leu Ser  
 115 120 125

Ser Ile Glu Glu Ala His Ala Tyr Ala Arg Leu Leu Glu Leu His Asp  
 130 135 140

Leu Thr Gln Glu Ala Leu Ala Gln Arg Leu Gly Lys Gly Gln Ser Thr  
 145 150 155 160

Ile Ala Asn Lys Leu Arg Leu Leu Lys Leu Pro Glu Glu Val Gln Glu  
 165 170 175

Ala Ile Leu Lys Lys Glu Ile Ser Glu Arg His Ala Arg Ala Leu Ile  
 180 185 190

Pro Leu Lys Gln Pro Asp Leu Gln Val Lys Leu Leu His Glu Val Ile  
 195 200 205

Glu Lys Ser Leu Asn Val Lys Gln Thr Glu Asp Arg Val Val Lys Met  
 210 215 220

Leu Glu Gln Asp Lys Arg Lys Pro Lys Pro Lys Arg Lys Ala Tyr Ser  
 225 230 235 240

Arg Asp Ala Arg Ile Ala Met Asn Thr Ile Arg Gln Ser Leu Ser Met  
 245 250 255

Val Glu Asp Ser Gly Val Lys Leu Asn Thr Glu Glu Glu Glu Phe Glu  
 260 265 270

Glu Tyr Ile Gln Phe Thr Ile Arg Ile Pro Lys  
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<210> 130  
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 ccggacacac ccacgcgcgg acaaattcag attcctgtat tcggtccttt gattacgcct 180  
 ccgtacgtag acgtttatac gcaaggaatg tatgcaacag ccggaatgaa aatttatgtc 240  
 atttgaggaa tcggcacgag caggctgccg ctccgctttc tgtcaaagcc tgaaatcacc 300  
 gtgttccagc ttgaatccat ttaatcttgc ccggtccttt ggctcaaaac aaaaggcatc 360  
 tgcatacatt aagtaaaaac attcccgtc catttcatcc aatcccatca aaaaaacgga 420  
 acttcctcag cctcttccgt ctatatatta gcagcggaaa aggctctctt ttcgtttttg 480  
 aaaaggagat gtgctgatta ttg ctg atg tac caa gtc aaa ccc gga gga acc 531  
 Leu Leu Met Tyr Gln Val Lys Pro Gly Gly Thr  
 1 5 10  
 ctt gaa agc atc gcc gcc gat ttc aga acg acc cgg cag gcg ttg ctg 581  
 Leu Glu Ser Ile Ala Ala Asp Phe Arg Thr Thr Arg Gln Ala Leu Leu

15	20	25	
cag gcg aat cct ggc tta aac ggc ggc caa gtg tcc gcg ggc cag tcg			629
Gln Ala Asn Pro Gly Leu Asn Gly Gly Gln Val Ser Ala Gly Gln Ser			
30	35	40	
att atc att ccc ggc atc aga aat ccg gac aca att cca tac cgg att			677
Ile Ile Ile Pro Gly Ile Arg Asn Pro Asp Thr Ile Pro Tyr Arg Ile			
45	50	55	
gcc gtg tct ctc aac gga aga acg ctc aga ttg tat gag cga gac aga			725
Ala Val Ser Leu Asn Gly Arg Thr Leu Arg Leu Tyr Glu Arg Asp Arg			
60	65	70	75
ctt gta aaa aca tat ccg att gcc gtc gga aaa atc ctc aca cag acg			773
Leu Val Lys Thr Tyr Pro Ile Ala Val Gly Lys Ile Leu Thr Gln Thr			
80	85	90	
ccg aga ggc gaa ttt gtc atc gtc aac cgg cag cca aat ccg ggc ggc			821
Pro Arg Gly Glu Phe Val Ile Val Asn Arg Gln Pro Asn Pro Gly Gly			
95	100	105	
ccg ttc ggc gcc tac tgg ctg agc ctg tca aaa cag cac tac ggc atc			869
Pro Phe Gly Ala Tyr Trp Leu Ser Leu Ser Lys Gln His Tyr Gly Ile			
110	115	120	
cat gga acg aat aac cct tcg tca att ggc aaa gct gtt tca agg gga			917
His Gly Thr Asn Asn Pro Ser Ser Ile Gly Lys Ala Val Ser Arg Gly			
125	130	135	
tgt atc cgc atg cac aat cgg gat gtt ctg gaa ctt gct tct atc gta			965
Cys Ile Arg Met His Asn Arg Asp Val Leu Glu Leu Ala Ser Ile Val			
140	145	150	155
ccc aac gga acc cga gtg tcc att aca cct tagacgagta catttccaga			1015
Pro Asn Gly Thr Arg Val Ser Ile Thr Pro			
160	165		
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ggagcgtata tatggatctt tttaaaaatc gtaatttcgt ccgacttttt ttcgcagctt			1135
tcgcttctca aatgggaacg acagtcggaa atatggcttt cgcctttttc ttgctcgacc			1195
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caaattatac cgcttggtgt tttagtccta tttatcagaa gcgcgggttac aaaatttttc			1435
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<212> PRT

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<400> 131

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Leu Asn Gly Gly Gln Val Ser Ala Gly Gln Ser Ile Ile Ile Pro Gly  
35 40 45

Ile Arg Asn Pro Asp Thr Ile Pro Tyr Arg Ile Ala Val Ser Leu Asn  
50 55 60

Gly Arg Thr Leu Arg Leu Tyr Glu Arg Asp Arg Leu Val Lys Thr Tyr  
65 70 75 80

Pro Ile Ala Val Gly Lys Ile Leu Thr Gln Thr Pro Arg Gly Glu Phe  
85 90 95

Val Ile Val Asn Arg Gln Pro Asn Pro Gly Gly Pro Phe Gly Ala Tyr  
100 105 110

Trp Leu Ser Leu Ser Lys Gln His Tyr Gly Ile His Gly Thr Asn Asn  
115 120 125

Pro Ser Ser Ile Gly Lys Ala Val Ser Arg Gly Cys Ile Arg Met His  
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Asn Arg Asp Val Leu Glu Leu Ala Ser Ile Val Pro Asn Gly Thr Arg  
145 150 155 160

Val Ser Ile Thr Pro  
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<210> 132

<211> 1897

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1397)

<400> 132

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cggctgtggc cggtcaagat gctgcctttt tctttcaagt cgtaaaagca agctttgcac      180
agcgctgaaa aacgcttttc aacaacctcg tcaacaatct gccgaatggc aaagagaata      240
aatcaaaaaat tgaaagagcg cttcaggatt cacatatcga cggaaaacga cgcggagagt      300
cgcttagcat tgaagagttc gccgtcttat ctgaccgctt gagagaagtc cttctttaat      360
ggaggggcttt ttttattgat gccgggcttt aagcctgac aggccttgta tccgttcacc      420
acttgaaggg caggcacata ggctaaagaa gcacctttac tttttcgttg cttgatgttc      480
atcaggatgg ggcttagtct atg tgt gga gtg aaa agc atg caa ttt aaa ata      533
                        Met Cys Gly Val Lys Ser Met Gln Phe Lys Ile
                        1             5             10

ggc gat atg gtc gtc aga aaa tct tat cga aga gat att tta ttt cga      581
Gly Asp Met Val Val Arg Lys Ser Tyr Arg Arg Asp Ile Leu Phe Arg
                        15             20             25

att ata aga att gat caa tcg gca aat gga gaa cct gta gcc gtt ttg      629
Ile Ile Arg Ile Asp Gln Ser Ala Asn Gly Glu Pro Val Ala Val Leu
                        30             35             40

cac gga gat gag gtc aga tta atc gct gac gcg cat ttg ggg gat ctt      677
His Gly Asp Glu Val Arg Leu Ile Ala Asp Ala His Leu Gly Asp Leu
                        45             50             55

gag att gtc cgc gag gct gag tgg cag atg aga aag cgg gaa gaa gaa      725
Glu Ile Val Arg Glu Ala Glu Trp Gln Met Arg Lys Arg Glu Glu Glu
60             65             70             75

acg aga atg aag gaa tcc ctc gat ctt ctc cgc cag gat tac aaa ctc      773
Thr Arg Met Lys Glu Ser Leu Asp Leu Leu Arg Gln Asp Tyr Lys Leu
                        80             85             90

ctt cac gat aaa cat gag tac cgc gcc aca aac caa tat aac aat caa      821
Leu His Asp Lys His Glu Tyr Arg Ala Thr Asn Gln Tyr Asn Asn Gln
                        95             100            105

cag cag tac ttt cat atg ccc gga aga gtc ctt cat tta gac ggg gat      869
Gln Gln Tyr Phe His Met Pro Gly Arg Val Leu His Leu Asp Gly Asp
110            115            120

tcg gct tat ttg aaa aag tgt ctg gcg ctc tac gaa aag atc ggg gtt      917
Ser Ala Tyr Leu Lys Lys Cys Leu Ala Leu Tyr Glu Lys Ile Gly Val
125            130            135

cct gta tac ggc att cat tgc tat gaa aag aaa atg tca tca gtc atc      965
Pro Val Tyr Gly Ile His Cys Tyr Glu Lys Lys Met Ser Ser Val Ile
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140	145	150	155	
gag gaa ctg atc gat gaa tac cgc ccg gat ctt ctc gtc att acc gga				1013
Glu Glu Leu Ile Asp Glu Tyr Arg Pro Asp Leu Leu Val Ile Thr Gly				
	160	165	170	
cac gat gcc tat tct aag cag aag ggc gat att aac aat ctg gat gcc				1061
His Asp Ala Tyr Ser Lys Gln Lys Gly Asp Ile Asn Asn Leu Asp Ala				
	175	180	185	
tac agg cat tca aaa gat ttt atc gaa acc gtt caa aaa gcg aga aga				1109
Tyr Arg His Ser Lys Asp Phe Ile Glu Thr Val Gln Lys Ala Arg Arg				
	190	195	200	
aaa att ccc cat ctt gat cag ctc gtc att ttt gcc ggc gca tgc cag				1157
Lys Ile Pro His Leu Asp Gln Leu Val Ile Phe Ala Gly Ala Cys Gln				
	205	210	215	
tcc cat ttt gaa tca ctg atc aga gcc ggt gca aat ttc gca agc tct				1205
Ser His Phe Glu Ser Leu Ile Arg Ala Gly Ala Asn Phe Ala Ser Ser				
	220	225	230	235
ccg tcc aga gtc aac atc cat gcg ctt gat ccg gtc tat ata gtc gca				1253
Pro Ser Arg Val Asn Ile His Ala Leu Asp Pro Val Tyr Ile Val Ala				
	240	245	250	
aaa atc agc ttc act ccg ttt atg gac cgc att aac gtc tgg gaa gtg				1301
Lys Ile Ser Phe Thr Pro Phe Met Asp Arg Ile Asn Val Trp Glu Val				
	255	260	265	
ctc aga aat acc ttg acg aga gaa aag ggg ctc gga ggt att gag acg				1349
Leu Arg Asn Thr Leu Thr Arg Glu Lys Gly Leu Gly Gly Ile Glu Thr				
	270	275	280	
cgg ggc gta ttg cgt att gga atg cca tat aaa aca aaa gca aac gat				1397
Arg Gly Val Leu Arg Ile Gly Met Pro Tyr Lys Thr Lys Ala Asn Asp				
	285	290	295	
taaacgagcc cgccggatgg cgggtttttg ctatgcacac gaaatgtttt tacctttttt				1457
ttaaaaaacat acataatgaa acgaaaaatg aggaaaataa gggaaagtcg gcgtataatt				1517
tgtcacaaat attttattga cagaggctta tgaacgttga tataatttaa attttatttg				1577
acaaaaatgg gcttctggtg tataactgaat atagtgaggt ggatgcaatg gcgaaaacgt				1637
tgtccgatat taaaagatcg cttgatggac atttgggaaa aaggctgacg ttaaaagcaa				1697
acggtggccg ccgaaaaacg attgagcgtt cgggcatttt agctgagacg tacccttctg				1757
tttttgtgat acaactagac caagacgaga attcgtttga aagagtttca tacagttatg				1817
cggatattct tactgagacg gttgaattga ggttttccga tgataaaacc agctcagtag				1877
ccctttaata agcagtggac				1897



<210> 133  
 <211> 299  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 133

Met Cys Gly Val Lys Ser Met Gln Phe Lys Ile Gly Asp Met Val Val  
 1 5 10 15

Arg Lys Ser Tyr Arg Arg Asp Ile Leu Phe Arg Ile Ile Arg Ile Asp  
 20 25 30

Gln Ser Ala Asn Gly Glu Pro Val Ala Val Leu His Gly Asp Glu Val  
 35 40 45

Arg Leu Ile Ala Asp Ala His Leu Gly Asp Leu Glu Ile Val Arg Glu  
 50 55 60

Ala Glu Trp Gln Met Arg Lys Arg Glu Glu Glu Thr Arg Met Lys Glu  
 65 70 75 80

Ser Leu Asp Leu Leu Arg Gln Asp Tyr Lys Leu Leu His Asp Lys His  
 85 90 95

Glu Tyr Arg Ala Thr Asn Gln Tyr Asn Asn Gln Gln Gln Tyr Phe His  
 100 105 110

Met Pro Gly Arg Val Leu His Leu Asp Gly Asp Ser Ala Tyr Leu Lys  
 115 120 125

Lys Cys Leu Ala Leu Tyr Glu Lys Ile Gly Val Pro Val Tyr Gly Ile  
 130 135 140

His Cys Tyr Glu Lys Lys Met Ser Ser Val Ile Glu Glu Leu Ile Asp  
 145 150 155 160

Glu Tyr Arg Pro Asp Leu Leu Val Ile Thr Gly His Asp Ala Tyr Ser  
 165 170 175

Lys Gln Lys Gly Asp Ile Asn Asn Leu Asp Ala Tyr Arg His Ser Lys  
 180 185 190

Asp Phe Ile Glu Thr Val Gln Lys Ala Arg Arg Lys Ile Pro His Leu  
 195 200 205

Asp Gln Leu Val Ile Phe Ala Gly Ala Cys Gln Ser His Phe Glu Ser  
 210 215 220

Leu Ile Arg Ala Gly Ala Asn Phe Ala Ser Ser Pro Ser Arg Val Asn  
 225 230 235 240

Ile His Ala Leu Asp Pro Val Tyr Ile Val Ala Lys Ile Ser Phe Thr  
 245 250 255

Pro Phe Met Asp Arg Ile Asn Val Trp Glu Val Leu Arg Asn Thr Leu  
 260 265 270

Thr Arg Glu Lys Gly Leu Gly Gly Ile Glu Thr Arg Gly Val Leu Arg  
 275 280 285

Ile Gly Met Pro Tyr Lys Thr Lys Ala Asn Asp  
 290 295

<210> 134  
 <211> 1010  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(734)

<400> 134  
 atcattaaag atatcgtgct ggggacgatg tcgaaaaaga atatggaaga aaagctggga 60  
 ttataaaaaa tcccggcttt tttgcttata ttgccccaaa aatggtgaaa atgaaaacaa 120  
 gctggagggtg attcaacatg aaaaaagcga aaaggcgaac atttgaagaa cttgtctcgg 180  
 aaaataaaaa ggagctcatg accaaccagg agtttcttga tcggctggaa gataagcttg 240  
 aagagaaatt taagctgaag tgagttttta aaaatcgatt catgttttacg ctcctttttg 300  
 agaatcctaa tgctgaaaag gagggataga catgccgaga gaacacgaca aacagtctaa 360  
 atttgccccg agccatcttg ggacaaaacc ggtagaatat aagcgcaaca aaggaaaaaa 420  
 gatgcatgat aaatcaggag aaacaccgat cattatgcag acaaaaggcg agtaaagatg 480  
 aaaaggaggc agagaccgga atg aca cat caa aaa cat cat ccg gat gac aga 533  
 Met Thr His Gln Lys His His Pro Asp Asp Arg  
 1 5 10

tca gac aac gta gaa aag ctt caa gac atg gtg cag aac aca atc gaa 581  
 Ser Asp Asn Val Glu Lys Leu Gln Asp Met Val Gln Asn Thr Ile Glu  
                   15                  20                  25

aac att gag gag tct gaa gag cag ctg tct ttt gcc agc gag gcg gaa 629  
 Asn Ile Glu Glu Ser Glu Glu Gln Leu Ser Phe Ala Ser Glu Ala Glu  
                   30                  35                  40

cag gaa cag atc cgc gaa aaa aat gaa cgc cga aat gaa agc att gag 677  
 Gln Glu Gln Ile Arg Glu Lys Asn Glu Arg Arg Asn Glu Ser Ile Glu  
                   45                  50                  55

gcg atg cgc aat gaa atc cat gac gag gcg gaa gcc cgc aaa aac gga 725  
 Ala Met Arg Asn Glu Ile His Asp Glu Ala Glu Ala Arg Lys Asn Gly  
                   60                  65                  70                  75

tat cat caa taaaccaggg cgacctggtt tttttgcatg aagcccgtcc 774  
 Tyr His Gln

gtcgtgtttt tgcccattgt atatgctaga attggattaa atacatttgt ggaaaaggga 834

gtagagggga aatttgtacg tctcaaaaaa agaaatagaa gtccgctatg ccgaaacaga 894

cccaaaatgg ggtgtcgtct atcacgccaa ttatttgatt ttgggatggg aggtaagccc 954

ggacggcttt aattaaagaa ctcggtttt ctttatgccg aaatgggaga aagacg 1010

<210> 135

<211> 78

<212> PRT

<213> Bacillus licheniformis

<400> 135

Met Thr His Gln Lys His His Pro Asp Asp Arg Ser Asp Asn Val Glu  
 1                  5                  10                  15

Lys Leu Gln Asp Met Val Gln Asn Thr Ile Glu Asn Ile Glu Glu Ser  
                   20                  25                  30

Glu Glu Gln Leu Ser Phe Ala Ser Glu Ala Glu Gln Glu Gln Ile Arg  
                   35                  40                  45

Glu Lys Asn Glu Arg Arg Asn Glu Ser Ile Glu Ala Met Arg Asn Glu  
                   50                  55                  60

Ile His Asp Glu Ala Glu Ala Arg Lys Asn Gly Tyr His Gln  
 65                  70                  75

<210> 136

<211> 2407  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1907)

<400> 136  
 gcatactgta aaaggccggg tgaatgaaga gcttttgaaa tcggtcgtga tagatccaaa 60  
 tggcgaattt tatgtatgcg gtccgctttc atttatgaaa agcgtgattg aaggattgca 120  
 aaaccttggc gtttcgatgg aaaacatccg ctatgagagc tttgcttcat ctcttgatat 180  
 gcaaatagcg aactaacctc aagaaggcag ctgtcaaacc gacagctgcc tcagcgtgtc 240  
 gacaaaccct cgcattgcgtt gtcagtcctg cgcgtcgggtg ctcacgaatt ccaacattcg 300  
 ctccgctccg atgctcggcc ttcctagact gcaagggttt tcaatcacgc tgaaagaagg 360  
 atgacaaaat cccaaaacta agagctgttt tgggattttg tcagcaatct aaggcagctg 420  
 tcaatccgac agctgccttt catcttttca aaacccggct catacaataa agagaagtcc 480  
 aaccgggggg gatttgagta ttg agc ata cgg gag caa aaa gag ctg cag cgg 533  
                                   Leu Ser Ile Arg Glu Gln Lys Glu Leu Gln Arg  
                                   1                                  5                                  10  
 gcg att gaa gaa att acg gaa atc gcg gaa gga ttc ggc ctt gat ttt 581  
 Ala Ile Glu Glu Ile Thr Glu Ile Ala Glu Gly Phe Gly Leu Asp Phe  
                                   15                                  20                                  25  
 tac ccg atg aga tat gag att tgt cct gct gaa att att tat aca ttc 629  
 Tyr Pro Met Arg Tyr Glu Ile Cys Pro Ala Glu Ile Ile Tyr Thr Phe  
                                   30                                  35                                  40  
 ggt gca tac ggg atg ccg aca aga tac agc cat tgg agt ttc gga aag 677  
 Gly Ala Tyr Gly Met Pro Thr Arg Tyr Ser His Trp Ser Phe Gly Lys  
                                   45                                  50                                  55  
 caa ttt cac aaa atg aag ctt cac tat gac ttt ggc ttg agc aaa ata 725  
 Gln Phe His Lys Met Lys Leu His Tyr Asp Phe Gly Leu Ser Lys Ile  
                                   60                                  65                                  70                                  75  
 tat gag ctt gtc att aat tca gat ccg tgt tat gcg ttt ttg ctg gac 773  
 Tyr Glu Leu Val Ile Asn Ser Asp Pro Cys Tyr Ala Phe Leu Leu Asp  
                                   80                                  85                                  90  
 agc aat tca ttg att caa aat aag ctg att gtc gca cac gtc ctt gct 821  
 Ser Asn Ser Leu Ile Gln Asn Lys Leu Ile Val Ala His Val Leu Ala  
                                   95                                  100                                  105  
 cat tgt gat ttc ttt aaa aat aac tgc cgt ttt caa aat acg aag cgc 869  
 His Cys Asp Phe Phe Lys Asn Asn Cys Arg Phe Gln Asn Thr Lys Arg  
                                   110                                  115                                  120

gat atg gtt gaa agc atg tcg gcg aca gca gag cgg att aaa cat tat	917
Asp Met Val Glu Ser Met Ser Ala Thr Ala Glu Arg Ile Lys His Tyr	
125 130 135	
gaa acg gta cac ggt tca aaa gaa gtc gaa gca ttt ctc gat gcg gtg	965
Glu Thr Val His Gly Ser Lys Glu Val Glu Ala Phe Leu Asp Ala Val	
140 145 150 155	
ctg gcg att gaa gaa cac att gac cct tcg ctc gtg agg ccg aag ctg	1013
Leu Ala Ile Glu Glu His Ile Asp Pro Ser Leu Val Arg Pro Lys Leu	
160 165 170	
tcg tgg agc gta gat gat gaa gag gaa gaa gaa acc ggc gcg ccg gcc	1061
Ser Trp Ser Val Asp Asp Glu Glu Glu Glu Glu Thr Gly Ala Pro Ala	
175 180 185	
act cct tat gac gac ctc tgg gaa ctg gat cat aaa gga tcg aaa gag	1109
Thr Pro Tyr Asp Asp Leu Trp Glu Leu Asp His Lys Gly Ser Lys Glu	
190 195 200	
aag aag aaa agg acg aaa aaa aag ttt ccg ccg aaa ccg gaa aaa gac	1157
Lys Lys Lys Arg Thr Lys Lys Lys Phe Pro Pro Lys Pro Glu Lys Asp	
205 210 215	
att ctg ctg ttc ata gaa gag cat tcg ccg gag ctg gag cct tgg cag	1205
Ile Leu Leu Phe Ile Glu Glu His Ser Arg Glu Leu Glu Pro Trp Gln	
220 225 230 235	
cgc gat att tta acg atg atg aga gag gaa atg ctg tat ttc tgg ccg	1253
Arg Asp Ile Leu Thr Met Met Arg Glu Glu Met Leu Tyr Phe Trp Pro	
240 245 250	
cag ctt gaa acg aaa atc atg aat gaa ggc tgg gcg tcc tat tgg cat	1301
Gln Leu Glu Thr Lys Ile Met Asn Glu Gly Trp Ala Ser Tyr Trp His	
255 260 265	
cag cga atc atc cgt gag ctt gat ctg aca tca agt gaa gcg atc gaa	1349
Gln Arg Ile Ile Arg Glu Leu Asp Leu Thr Ser Ser Glu Ala Ile Glu	
270 275 280	
ttc gcc aag ctg aac gcg gga gtg gtt cag ccg tcc aaa acg gga atc	1397
Phe Ala Lys Leu Asn Ala Gly Val Val Gln Pro Ser Lys Thr Gly Ile	
285 290 295	
aat cct tat tat ctc gga ttg aaa ata ttt gag gac ata gag gag cgc	1445
Asn Pro Tyr Tyr Leu Gly Leu Lys Ile Phe Glu Asp Ile Glu Glu Arg	
300 305 310 315	
tac aac aac ccg aca gaa gac atg aaa aag atg ggg gta gag ccg aac	1493
Tyr Asn Asn Pro Thr Glu Asp Met Lys Lys Met Gly Val Glu Pro Asn	
320 325 330	
tct ggg aga gaa aaa ata ttt gaa gtc agg gag atc gaa tca gac att	1541
Ser Gly Arg Glu Lys Ile Phe Glu Val Arg Glu Ile Glu Ser Asp Ile	
335 340 345	

tca ttt atc agg aac tat tta acg aag gat ctt gtg atg cgg gaa gac Ser Phe Ile Arg Asn Tyr Leu Thr Lys Asp Leu Val Met Arg Glu Asp 350 355 360	1589
ctc tac ttg ttt caa aaa cag gga agg gat tat aaa atc gtc gac aag Leu Tyr Leu Phe Gln Lys Gln Gly Arg Asp Tyr Lys Ile Val Asp Lys 365 370 375	1637
gat tgg gag gct gtg cgc gat cag ctt gtc agc atg aga gtc aac gga Asp Trp Glu Ala Val Arg Asp Gln Leu Val Ser Met Arg Val Asn Gly 380 385 390 395	1685
gga ttt cct tat ttg aca gtt gag gac gga gat tac tta aag aac aat Gly Phe Pro Tyr Leu Thr Val Glu Asp Gly Asp Tyr Leu Lys Asn Asn 400 405 410	1733
gaa tta tac atc aag cat tgg tat gaa ggg atc gaa ctc gat ttg aag Glu Leu Tyr Ile Lys His Trp Tyr Glu Gly Ile Glu Leu Asp Leu Lys 415 420 425	1781
tat ctt gaa aaa gtt ctg cct tac ctc cac cag cta tgg gga aga agc Tyr Leu Glu Lys Val Leu Pro Tyr Leu His Gln Leu Trp Gly Arg Ser 430 435 440	1829
gtg cat gtc gag acc gtg ctc gaa gat aaa ccc gtc atg ttt tcc tat Val His Val Glu Thr Val Leu Glu Asp Lys Pro Val Met Phe Ser Tyr 445 450 455	1877
gat gga aag gct gtc cac cgc aga tat tta taaaggctgc attttggcag Asp Gly Lys Ala Val His Arg Arg Tyr Leu 460 465	1927
ccttttttct tttaaagcgc aacgatttca actcgtccgt cctttcaaaa gaaatgccaa	1987
attaatgcac gtttgcccag ttttacgact tcattataaa aatgtaaaat aaagtattta	2047
atgatatttc taaaattgta atttttagctg ccggaaagcg taaaaatgta gtatttaagt	2107
tacctttgaa atgtaaatga aatattatct acccttaaaa acttttttttg aaaacgaata	2167
attaaggaat ttgacatagt aagtcaagac tatacctgat ggaattccct ccttataata	2227
gaagcagagg aagggctgaa gcagccgttc tcaaaaaaat gaaactgcta attttcgcct	2287
ttgaaaatat aaaatattct gctattggga ggacaacatg aaaaaacaag taataacagc	2347
agcatcagcg gttgttttag gatcgacttt gtttgcggga gccgcttccg cgcaaaccat	2407

<210> 137

<211> 469

<212> PRT

<213> Bacillus licheniformis

<400> 137

Leu Ser Ile Arg Glu Gln Lys Glu Leu Gln Arg Ala Ile Glu Glu Ile

1	5	10	15
Thr Glu Ile	Ala Glu Gly Phe Gly	Leu Asp Phe Tyr Pro	Met Arg Tyr
	20	25	30
Glu Ile Cys	Pro Ala Glu Ile Ile	Tyr Thr Phe Gly	Ala Tyr Gly Met
	35	40	45
Pro Thr Arg	Tyr Ser His Trp Ser	Phe Gly Lys Gln	Phe His Lys Met
	50	55	60
Lys Leu His	Tyr Asp Phe Gly	Leu Ser Lys Ile	Tyr Glu Leu Val Ile
65	70	75	80
Asn Ser Asp	Pro Cys Tyr Ala	Phe Leu Leu Asp	Ser Asn Ser Leu Ile
	85	90	95
Gln Asn Lys	Leu Ile Val Ala	His Val Leu Ala	His Cys Asp Phe Phe
	100	105	110
Lys Asn Asn	Cys Arg Phe Gln	Asn Thr Lys Arg	Asp Met Val Glu Ser
	115	120	125
Met Ser Ala	Thr Ala Glu Arg	Ile Lys His Tyr	Glu Thr Val His Gly
	130	135	140
Ser Lys Glu	Val Glu Ala Phe	Leu Asp Ala Val	Leu Ala Ile Glu Glu
145	150	155	160
His Ile Asp	Pro Ser Leu Val	Arg Pro Lys Leu	Ser Trp Ser Val Asp
	165	170	175
Asp Glu Glu	Glu Glu Glu Thr	Gly Ala Pro Ala	Thr Pro Tyr Asp Asp
	180	185	190
Leu Trp Glu	Leu Asp His Lys	Gly Ser Lys Glu	Lys Lys Arg Thr
	195	200	205
Lys Lys Lys	Phe Pro Pro Lys	Pro Glu Lys Asp	Ile Leu Leu Phe Ile
	210	215	220
Glu Glu His	Ser Arg Glu Leu	Glu Pro Trp Gln	Arg Asp Ile Leu Thr
225	230	235	240

Met Met Arg Glu Glu Met Leu Tyr Phe Trp Pro Gln Leu Glu Thr Lys  
245 250 255

Ile Met Asn Glu Gly Trp Ala Ser Tyr Trp His Gln Arg Ile Ile Arg  
260 265 270

Glu Leu Asp Leu Thr Ser Ser Glu Ala Ile Glu Phe Ala Lys Leu Asn  
275 280 285

Ala Gly Val Val Gln Pro Ser Lys Thr Gly Ile Asn Pro Tyr Tyr Leu  
290 295 300

Gly Leu Lys Ile Phe Glu Asp Ile Glu Glu Arg Tyr Asn Asn Pro Thr  
305 310 315 320

Glu Asp Met Lys Lys Met Gly Val Glu Pro Asn Ser Gly Arg Glu Lys  
325 330 335

Ile Phe Glu Val Arg Glu Ile Glu Ser Asp Ile Ser Phe Ile Arg Asn  
340 345 350

Tyr Leu Thr Lys Asp Leu Val Met Arg Glu Asp Leu Tyr Leu Phe Gln  
355 360 365

Lys Gln Gly Arg Asp Tyr Lys Ile Val Asp Lys Asp Trp Glu Ala Val  
370 375 380

Arg Asp Gln Leu Val Ser Met Arg Val Asn Gly Gly Phe Pro Tyr Leu  
385 390 395 400

Thr Val Glu Asp Gly Asp Tyr Leu Lys Asn Asn Glu Leu Tyr Ile Lys  
405 410 415

His Trp Tyr Glu Gly Ile Glu Leu Asp Leu Lys Tyr Leu Glu Lys Val  
420 425 430

Leu Pro Tyr Leu His Gln Leu Trp Gly Arg Ser Val His Val Glu Thr  
435 440 445

Val Leu Glu Asp Lys Pro Val Met Phe Ser Tyr Asp Gly Lys Ala Val  
450 455 460



His Arg Arg Tyr Leu  
465

<210> 138  
<211> 1291  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(791)

<400> 138  
ggaattgttg tcaacaatat gttttacagt tcggggcaaa ttccgctgac cccgtcgggt 60  
gaaatggtga ctggagacat cacagaacag acgcaccagg ttttccgcaa tttaaaagcc 120  
gtgctgaaaag aagcggggcgc ctctctggag actgtcgtca aagcaaccgt gtttctggcg 180  
gatatgaatc aattcacaga ggtgaatgaa gtttacggac agtacttcga taccacaaaa 240  
ccggcgagat catgcgttga ggtggcgagg ctgccgaaaag acgcgcttgt tgaaatagaa 300  
gtcatcgcac tagtgaaata gaaagaactc ttaaaagatg gttttggtct caaaatcatc 360  
ttttttgttt ggaaaatttg tcaattcagt gtttttttat cccaatatta caaaaatatt 420  
tttaattatg caggaaaaca aaaaaagccg ttgaatagtt acactaatgt ttttatattg 480  
ggaaaagggtg gtgaactact gtg gaa gtt acc gac gta aga tta cgc cgc gtg 533  
Val Glu Val Thr Asp Val Arg Leu Arg Arg Val  
1 5 10  
aat acc gat ggt cgc atg aga gcg att gca tcc atc acg ctg gat cac 581  
Asn Thr Asp Gly Arg Met Arg Ala Ile Ala Ser Ile Thr Leu Asp His  
15 20 25  
gaa ttt gta gtg cat gat att cgt gta att gat gga aac aat ggt ctt 629  
Glu Phe Val Val His Asp Ile Arg Val Ile Asp Gly Asn Asn Gly Leu  
30 35 40  
ttc gtt gcg atg cca agt aag cgt aca cct gat gga gaa ttt cgt gat 677  
Phe Val Ala Met Pro Ser Lys Arg Thr Pro Asp Gly Glu Phe Arg Asp  
45 50 55  
atc gct cat cca atc aac tca agc acc cgc gga aaa att cag gac gcg 725  
Ile Ala His Pro Ile Asn Ser Ser Thr Arg Gly Lys Ile Gln Asp Ala  
60 65 70 75  
gtg tta aat gaa tat cat cgt ttg ggt gac gtt gag gaa ata gaa tat 773  
Val Leu Asn Glu Tyr His Arg Leu Gly Asp Val Glu Glu Ile Glu Tyr  
80 85 90  
gaa gaa att gga gct tct taaaaaagaa gggcttatgg ataagccctt 821

Glu Glu Ile Gly Ala Ser  
95

tttgttttga aaaaaaatga tcttatcata ataaaatgac aatatatggt ttgtgtctgc 881  
gtataacagt agcaggaagg taaagcatgc gaactcggat aacaaagcgc atgcagaagg 941  
aatcaatccg tctccctgat cagttaatcc taaatatgct ctaaacaatcc aaaatatgct 1001  
gtcttgattt cccgatttct cattttggct tgcttgaaat caactcatat ttaggatata 1061  
tttttctatg gataataggg ataatggagg ccaatacatg gataagcggg ttgcagttgt 1121  
gttagcagct ggtcaaggaa caagaatgaa atcaaagcta tataaagttc ttcacacctgt 1181  
ttgcggaaaa cctatgggtcg agcatgttgt cgatgaagct cgcaagctat cattagaaaa 1241  
actgtgcaca atagttggac atggtgcgga agatgtcaaa aaacagctcg 1291

<210> 139  
<211> 97  
<212> PRT  
<213> Bacillus licheniformis

<400> 139

Val Glu Val Thr Asp Val Arg Leu Arg Arg Val Asn Thr Asp Gly Arg  
1 5 10 15

Met Arg Ala Ile Ala Ser Ile Thr Leu Asp His Glu Phe Val Val His  
20 25 30

Asp Ile Arg Val Ile Asp Gly Asn Asn Gly Leu Phe Val Ala Met Pro  
35 40 45

Ser Lys Arg Thr Pro Asp Gly Glu Phe Arg Asp Ile Ala His Pro Ile  
50 55 60

Asn Ser Ser Thr Arg Gly Lys Ile Gln Asp Ala Val Leu Asn Glu Tyr  
65 70 75 80

His Arg Leu Gly Asp Val Glu Glu Ile Glu Tyr Glu Glu Ile Gly Ala  
85 90 95

Ser

<210> 140  
<211> 1694

<212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1451)

<400> 140  
 gctcgcgagggg gatgcgcgttt cgtcaaccct taaaaacgcc cgatatctgc cggaatggct 60  
 gaagctgcaa aaggaaatta aacaagagat tgaaaaagcg atcaaatacga atcagcgcga 120  
 aacgctgatt gatgccatca accaaaaaat taaaaaatac aacctcacct gtccgaacca 180  
 attccaaaaa ggccttgttt cagccaaaaa cctcgaaaagt cagctcaaatt attggagctg 240  
 atgccattcc ctgcacttat tcataaaaaat aattgccaat aacaatcatc ttatgtaaaa 300  
 taaaggtaat atttatgctt ttaaaaagga gaaaggatga atgaagaagt ggaagcgaaa 360  
 gcggcatatc gaaaagcggc ctggctcctg aatcagtggg acaccatgat caagcgccat 420  
 gaagcgcctc aggctgtatc tttgaggtac gagatccaaa acctgctttc taaaatggag 480  
 aaaagcggag atctggagct ttg ttt tca gct gtt gga cta tcg ctg caa att 533  
 Leu Phe Ser Ala Val Gly Leu Ser Leu Gln Ile  
 1 5 10  
 gat gat gga gca gtt tca gaa tca gcc gag ctt ttc cgg aaa att aaa 581  
 Asp Asp Gly Ala Val Ser Glu Ser Ala Glu Leu Phe Arg Lys Ile Lys  
 15 20 25  
 agg cag aag gaa acg gtt aag agc gcg gat gac atc att cag tac tat 629  
 Arg Gln Lys Glu Thr Val Lys Ser Ala Asp Asp Ile Ile Gln Tyr Tyr  
 30 35 40  
 ttt ttc ttt ttt tca ggc atg tat gag ttt tat gag aaa aac tat ttt 677  
 Phe Phe Phe Phe Ser Gly Met Tyr Glu Phe Tyr Glu Lys Asn Tyr Phe  
 45 50 55  
 gag gcg atc agc tgt tac aag aaa gcg gaa gcg aag ctg cat aaa ctg 725  
 Glu Ala Ile Ser Cys Tyr Lys Lys Ala Glu Ala Lys Leu His Lys Leu  
 60 65 70 75  
 acc gat gaa att gaa aaa gcg gaa ttt tat tat aaa atc gcg acc gcc 773  
 Thr Asp Glu Ile Glu Lys Ala Glu Phe Tyr Tyr Lys Ile Ala Thr Ala  
 80 85 90  
 tac tac caa ata gac gat cat ttc aga tcg ttg aac tac tcc gaa aaa 821  
 Tyr Tyr Gln Ile Asp Asp His Phe Arg Ser Leu Asn Tyr Ser Glu Lys  
 95 100 105  
 gcg ctc tca ctt ttc agc aag cat aaa gaa tac ata gac aaa acg atc 869  
 Ala Leu Ser Leu Phe Ser Lys His Lys Glu Tyr Ile Asp Lys Thr Ile  
 110 115 120

gga tgc gaa atg ata ctc gga tcg gtg cag ttt gaa ttg ttc cgc atc Gly Cys Glu Met Ile Leu Gly Ser Val Gln Phe Glu Leu Phe Arg Ile 125 130 135	917
aaa caa gct gag gag cac tac ggg cgg gcg ctt gat cag gcc gtt gcc Lys Gln Ala Glu Glu His Tyr Gly Arg Ala Leu Asp Gln Ala Val Ala 140 145 150 155	965
ctt caa aac cgg cga atc atc ggg ctg atc tat cat aat atg gga ctg Leu Gln Asn Arg Arg Ile Ile Gly Leu Ile Tyr His Asn Met Gly Leu 160 165 170	1013
aac tat gcc aaa tgc ggc atg ccg ctt ttg gcg gag gag cac ttt aga Asn Tyr Ala Lys Cys Gly Met Pro Leu Leu Ala Glu Glu His Phe Arg 175 180 185	1061
aaa gcc ctt tca atc ggt gtc cat gag caa tcg gtt ttt ggc att aac Lys Ala Leu Ser Ile Gly Val His Glu Gln Ser Val Phe Gly Ile Asn 190 195 200	1109
acc ctt ttc gag ctg tct cac ctc atg tac aaa aac ggt tct ccc gaa Thr Leu Phe Glu Leu Ser His Leu Met Tyr Lys Asn Gly Ser Pro Glu 205 210 215	1157
gaa gcg aga cgt ctc tgc aaa gag gga ttt acc aga tcg gcc gaa tta Glu Ala Arg Arg Leu Cys Lys Glu Gly Phe Thr Arg Ser Ala Glu Leu 220 225 230 235	1205
gga gag gat gaa tac gca gcg aag ttc agg ctg att ttc gcc ctg tat Gly Glu Asp Glu Tyr Ala Ala Lys Phe Arg Leu Ile Phe Ala Leu Tyr 240 245 250	1253
gac gct ggc cat ccg ctc gat att gaa ttt tcg ctt gaa tat atg agt Asp Ala Gly His Pro Leu Asp Ile Glu Phe Ser Leu Glu Tyr Met Ser 255 260 265	1301
gat aaa cgg cta tgg ccg cat gtt gct gaa ctg aca aaa gat att gcc Asp Lys Arg Leu Trp Pro His Val Ala Glu Leu Thr Lys Asp Ile Ala 270 275 280	1349
gac tat tac atg aag tca ggc gac cat gaa aaa agc gcg ctt tac ctg Asp Tyr Tyr Met Lys Ser Gly Asp His Glu Lys Ser Ala Leu Tyr Leu 285 290 295	1397
gaa aaa tcg cag cat gcg aaa aat caa ata tat aaa atg aag gag ggg Glu Lys Ser Gln His Ala Lys Asn Gln Ile Tyr Lys Met Lys Glu Gly 300 305 310 315	1445
att ata tgaaaaaaaaa catttgtttt ttccgcgtca tgcttgtttg cctgatgggg Ile Ile	1501
ggaagcttca cagctgattc tgcagcacag gacggatcgt ttcagccatt gggaaagtcg	1561
gtgttttcctg ccagcggacg atagagataa cttgccgaga tagaaatggc ctcccgtctt	1621
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gatttcgcgc tgc

1694

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<211> 317  
<212> PRT  
<213> Bacillus licheniformis

<400> 141

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Ser Glu Ser Ala Glu Leu Phe Arg Lys Ile Lys Arg Gln Lys Glu Thr  
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Val Lys Ser Ala Asp Asp Ile Ile Gln Tyr Tyr Phe Phe Phe Phe Ser  
35 40 45

Gly Met Tyr Glu Phe Tyr Glu Lys Asn Tyr Phe Glu Ala Ile Ser Cys  
50 55 60

Tyr Lys Lys Ala Glu Ala Lys Leu His Lys Leu Thr Asp Glu Ile Glu  
65 70 75 80

Lys Ala Glu Phe Tyr Tyr Lys Ile Ala Thr Ala Tyr Tyr Gln Ile Asp  
85 90 95

Asp His Phe Arg Ser Leu Asn Tyr Ser Glu Lys Ala Leu Ser Leu Phe  
100 105 110

Ser Lys His Lys Glu Tyr Ile Asp Lys Thr Ile Gly Cys Glu Met Ile  
115 120 125

Leu Gly Ser Val Gln Phe Glu Leu Phe Arg Ile Lys Gln Ala Glu Glu  
130 135 140

His Tyr Gly Arg Ala Leu Asp Gln Ala Val Ala Leu Gln Asn Arg Arg  
145 150 155 160

Ile Ile Gly Leu Ile Tyr His Asn Met Gly Leu Asn Tyr Ala Lys Cys  
165 170 175

Gly Met Pro Leu Leu Ala Glu Glu His Phe Arg Lys Ala Leu Ser Ile  
180 185 190

Gly Val His Glu Gln Ser Val Phe Gly Ile Asn Thr Leu Phe Glu Leu  
 195 200 205

Ser His Leu Met Tyr Lys Asn Gly Ser Pro Glu Glu Ala Arg Arg Leu  
 210 215 220

Cys Lys Glu Gly Phe Thr Arg Ser Ala Glu Leu Gly Glu Asp Glu Tyr  
 225 230 235 240

Ala Ala Lys Phe Arg Leu Ile Phe Ala Leu Tyr Asp Ala Gly His Pro  
 245 250 255

Leu Asp Ile Glu Phe Ser Leu Glu Tyr Met Ser Asp Lys Arg Leu Trp  
 260 265 270

Pro His Val Ala Glu Leu Thr Lys Asp Ile Ala Asp Tyr Tyr Met Lys  
 275 280 285

Ser Gly Asp His Glu Lys Ser Ala Leu Tyr Leu Glu Lys Ser Gln His  
 290 295 300

Ala Lys Asn Gln Ile Tyr Lys Met Lys Glu Gly Ile Ile  
 305 310 315

<210> 142  
 <211> 1260  
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 actcaaaatc gtgttccttc gggagtgtcg gttcgacccc gaccaccggt atcactaaac 180  
 atcgtattgc caaacgatga aagagcgttc ctacaaaagg agcgctcttt ttatttatc 240  
 cttatcttgg aacgaagccg taagaatttt ttcttaagga ctgcgagctc cggaagctac 300  
 gggaacatac cgtgagattt atcgaaatga gcttaatacg gtgcagaaac ttttacaaaa 360

gcaaaaatat atctgatgat ttattatcta tttatagggc gaaaagtaaa ttattgatac	420
aaacttcttt gcaaagattg gtaactttct gtaaaatggt ctcatagcga tagaggcagt	480
aaagtgtggg aggtttgaca atg aaa gca gca gcc tct gtg aac gta gcc aat	533
Met Lys Ala Ala Ala Ser Val Asn Val Ala Asn	
1 5 10	
ctc atc aat cag tgg tat gtt cac ata aaa aag aga gat gtt tca aat	581
Leu Ile Asn Gln Trp Tyr Val His Ile Lys Lys Arg Asp Val Ser Asn	
15 20 25	
gcc gta gaa ctt agg gac aga ata aaa ggc ctt tta aac gta atg gaa	629
Ala Val Glu Leu Arg Asp Arg Ile Lys Gly Leu Leu Asn Val Met Glu	
30 35 40	
gaa gat cag gat gtt ttg ctt tac ttt aat cta ctt gat tac agg ttc	677
Glu Asp Gln Asp Val Leu Leu Tyr Phe Asn Leu Leu Asp Tyr Arg Phe	
45 50 55	
aga gta tta atg gaa gac gtc gcg ggg gag ccg cag ctt ccg cct att	725
Arg Val Leu Met Glu Asp Val Ala Gly Glu Pro Gln Leu Pro Pro Ile	
60 65 70 75	
gct gaa gat aag gcg aag aca gac ggt ttg tta cga tac tat tac ttt	773
Ala Glu Asp Lys Ala Lys Thr Asp Gly Leu Leu Arg Tyr Tyr Tyr Phe	
80 85 90	
ctc ttt aaa gga atg tat gaa agt gcg agg agc aac tac tct aaa gcg	821
Leu Phe Lys Gly Met Tyr Glu Ser Ala Arg Ser Asn Tyr Ser Lys Ala	
95 100 105	
ctt aat tgt ttt aga gtt gcc gag cgg cag ctc gat aat gtc gaa gat	869
Leu Asn Cys Phe Arg Val Ala Glu Arg Gln Leu Asp Asn Val Glu Asp	
110 115 120	
gaa atc gaa aag gcc gag ttt cat tat aag ctt gga aat ctc tat tat	917
Glu Ile Glu Lys Ala Glu Phe His Tyr Lys Leu Gly Asn Leu Tyr Tyr	
125 130 135	
ttt acg aaa aca act cta ctt tct ttt cat cat ctt tca atc gcg aag	965
Phe Thr Lys Thr Thr Leu Leu Ser Phe His His Leu Ser Ile Ala Lys	
140 145 150 155	
agc att tat agg gct tat gaa gaa tat aag aca cag tcg ata aac tgt	1013
Ser Ile Tyr Arg Ala Tyr Glu Glu Tyr Lys Thr Gln Ser Ile Asn Cys	
160 165 170	
acg gtg ctg ctc gca ctc aat tat ata gac gac gga cgt tta aca aga	1061
Thr Val Leu Leu Ala Leu Asn Tyr Ile Asp Asp Gly Arg Leu Thr Arg	
175 180 185	
gct gaa aat atg ctt aag agt tgc gca gaa aga ctg atc aag atg ggc	1109
Ala Glu Asn Met Leu Lys Ser Cys Ala Glu Arg Leu Ile Lys Met Gly	
190 195 200	
gat aat cat ctg ctg gcg gct gtc tac tat gat ctc ggc ttt tta aaa	1157

Asp Asn His Leu Leu Ala Ala Val Tyr Tyr Asp Leu Gly Phe Leu Lys  
 205 210 215  
 att caa gag gat aaa cat gaa gaa gca ctc gag tat ttc gac ctc tca 1205  
 Ile Gln Glu Asp Lys His Glu Glu Ala Leu Glu Tyr Phe Asp Leu Ser  
 220 225 230 235  
 ttt aaa acg ggt gat atc gaa aaa aat gag ccg ggg act tagctcgata 1254  
 Phe Lys Thr Gly Asp Ile Glu Lys Asn Glu Pro Gly Thr  
 240 245  
 gatgta 1260

<210> 143  
 <211> 248  
 <212> PRT  
 <213> Bacillus licheniformis  
 <400> 143

Met Lys Ala Ala Ala Ser Val Asn Val Ala Asn Leu Ile Asn Gln Trp  
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Tyr Val His Ile Lys Lys Arg Asp Val Ser Asn Ala Val Glu Leu Arg  
 20 25 30

Asp Arg Ile Lys Gly Leu Leu Asn Val Met Glu Glu Asp Gln Asp Val  
 35 40 45

Leu Leu Tyr Phe Asn Leu Leu Asp Tyr Arg Phe Arg Val Leu Met Glu  
 50 55 60

Asp Val Ala Gly Glu Pro Gln Leu Pro Pro Ile Ala Glu Asp Lys Ala  
 65 70 75 80

Lys Thr Asp Gly Leu Leu Arg Tyr Tyr Tyr Phe Leu Phe Lys Gly Met  
 85 90 95

Tyr Glu Ser Ala Arg Ser Asn Tyr Ser Lys Ala Leu Asn Cys Phe Arg  
 100 105 110

Val Ala Glu Arg Gln Leu Asp Asn Val Glu Asp Glu Ile Glu Lys Ala  
 115 120 125

Glu Phe His Tyr Lys Leu Gly Asn Leu Tyr Tyr Phe Thr Lys Thr Thr  
 130 135 140



Leu Leu Ser Phe His His Leu Ser Ile Ala Lys Ser Ile Tyr Arg Ala  
 145 150 155 160

Tyr Glu Glu Tyr Lys Thr Gln Ser Ile Asn Cys Thr Val Leu Leu Ala  
 165 170 175

Leu Asn Tyr Ile Asp Asp Gly Arg Leu Thr Arg Ala Glu Asn Met Leu  
 180 185 190

Lys Ser Cys Ala Glu Arg Leu Ile Lys Met Gly Asp Asn His Leu Leu  
 195 200 205

Ala Ala Val Tyr Tyr Asp Leu Gly Phe Leu Lys Ile Gln Glu Asp Lys  
 210 215 220

His Glu Glu Ala Leu Glu Tyr Phe Asp Leu Ser Phe Lys Thr Gly Asp  
 225 230 235 240

Ile Glu Lys Asn Glu Pro Gly Thr  
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<210> 144  
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 <212> DNA  
 <213> Bacillus licheniformis

<220>  
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<400> 144  
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 gtgtaccgca gatataatct attgcctatc gatttttctaa aaggcgtaga aatgtatctg 180  
 cggtttttttc tttagctttt tatttcataa aagagggttg aatttttgctt cctaacgatt 240  
 agttatgcca aattacatat caacaggaaa atataatcct tcatctgttc tgccttcctt 300  
 cctatacttc taaaattcac ccaaacacgg aaaacgaatc atattgatta ggccaaaaaa 360  
 cctctaactt ataaagattt ctgagaatgt tgttggtgaaa aattattact tttatgtaaa 420  
 atgatgacta tgaataaaaa gggaattgct attttgggtt tttagaaaaa ttataatctt 480  
 gcgagaaagg aagaggatat gtg agc gtg ata cca tat gat ttg gtt gcg acg 533  
 Val Ser Val Ile Pro Tyr Asp Leu Val Ala Thr

	1	5	10	
aaa atg aat ttt tgg tat aca gcc tta aaa aac aat tgg aca ggc aag				581
Lys Met Asn Phe Trp Tyr Thr Ala Leu Lys Asn Asn Trp Thr Gly Lys	15	20	25	
gct gag gat act aag aaa gaa gtt gaa cga gaa tta gaa caa atg gaa				629
Ala Glu Asp Thr Lys Lys Glu Val Glu Arg Glu Leu Glu Gln Met Glu	30	35	40	
caa aat cag gat gtg att gtc tat tac aac tta ctg ctc ttc cgg cat				677
Gln Asn Gln Asp Val Ile Val Tyr Tyr Asn Leu Leu Leu Phe Arg His	45	50	55	
aat ctt caa ctt gat tat atg tat tct aaa ccc ggt gta aat tta aat				725
Asn Leu Gln Leu Asp Tyr Met Tyr Ser Lys Pro Gly Val Asn Leu Asn	60	65	70	75
agt cgt ttt gat gag ttc aaa aag att cgc gat cag aat aat ctg gaa				773
Ser Arg Phe Asp Glu Phe Lys Lys Ile Arg Asp Gln Asn Asn Leu Glu	80	85	90	
gga atg ttg gat tat tat tat cat ttt ttc gct gga atg tat cat ttc				821
Gly Met Leu Asp Tyr Tyr Tyr His Phe Phe Ala Gly Met Tyr His Phe	95	100	105	
aga caa aaa gaa tta atc ctt gcg ctg aat ttt tat agg gat gcc gag				869
Arg Gln Lys Glu Leu Ile Leu Ala Leu Asn Phe Tyr Arg Asp Ala Glu	110	115	120	
aaa aaa ctc gat tct ttt gat tgt gat gaa ctg gaa aag gct gaa ttt				917
Lys Lys Leu Asp Ser Phe Asp Cys Asp Glu Leu Glu Lys Ala Glu Phe	125	130	135	
tat ttc aag gca tct gaa gtg tat tac cat atg aaa caa acc atc ttt				965
Tyr Phe Lys Ala Ser Glu Val Tyr Tyr His Met Lys Gln Thr Ile Phe	140	145	150	155
tcg atg aat tat gca agt cgt gcg tat aac tta ttc aaa aag tat gat				1013
Ser Met Asn Tyr Ala Ser Arg Ala Tyr Asn Leu Phe Lys Lys Tyr Asp	160	165	170	
act tac ggt gag cgt cga gta caa agt cag ttt att att gca ggt aac				1061
Thr Tyr Gly Glu Arg Arg Val Gln Ser Gln Phe Ile Ile Ala Gly Asn	175	180	185	
tgg cta gat cat atg tat ccc gaa aaa gct cta cat aat tta aat aaa				1109
Trp Leu Asp His Met Tyr Pro Glu Lys Ala Leu His Asn Leu Asn Lys	190	195	200	
gag ctt aaa gag tca gag aca caa gga att ctt cat ctt atg ggt tca				1157
Glu Leu Lys Glu Ser Glu Thr Gln Gly Ile Leu His Leu Met Gly Ser	205	210	215	
tca cat tta aat atc gga ata tgc tac aat aaa ttg gaa gat gtc gat				1205
Ser His Leu Asn Ile Gly Ile Cys Tyr Asn Lys Leu Glu Asp Val Asp	220	225	230	235

aaa gca acc tac aat ttt caa aga gct ctg aac ctt tat aaa gag gag	1253
Lys Ala Thr Tyr Asn Phe Gln Arg Ala Leu Asn Leu Tyr Lys Glu Glu	
240 245 250	
aag cat agt ttt ttg cca aaa aca tta ttc aac ctc gca cat gtc agg	1301
Lys His Ser Phe Leu Pro Lys Thr Leu Phe Asn Leu Ala His Val Arg	
255 260 265	
gca aag caa ggg aag ttg tca ata act gat gac cta tac tat gaa ggc	1349
Ala Lys Gln Gly Lys Leu Ser Ile Thr Asp Asp Leu Tyr Tyr Glu Gly	
270 275 280	
aaa gag ttg gct gaa aag aac aag aat tta gat atg ctt gca aag ttt	1397
Lys Glu Leu Ala Glu Lys Asn Lys Asn Leu Asp Met Leu Ala Lys Phe	
285 290 295	
gat tta ata aaa ggg ctt tat ctt tca ttt gat ctg gat atg gtt cgc	1445
Asp Leu Ile Lys Gly Leu Tyr Leu Ser Phe Asp Leu Asp Met Val Arg	
300 305 310 315	
gaa tcg ttc aag ttt ttc gaa agt aaa ggc aag tat gca gac atg gag	1493
Glu Ser Phe Lys Phe Phe Glu Ser Lys Gly Lys Tyr Ala Asp Met Glu	
320 325 330	
gaa tac ggt ctt ata gcg gct gaa cta tta gag aaa aaa gaa aaa att	1541
Glu Tyr Gly Leu Ile Ala Ala Glu Leu Leu Glu Lys Lys Glu Lys Ile	
335 340 345	
cga gat gca gtg gaa ttc tac cgg ata aca gtt aat gcg aga aga caa	1589
Arg Asp Ala Val Glu Phe Tyr Arg Ile Thr Val Asn Ala Arg Arg Gln	
350 355 360	
att caa agg agt gct ttt cta cat gta aac taaatcggtc taggggtagt	1639
Ile Gln Arg Ser Ala Phe Leu His Val Asn	
365 370	
taaagcagca ggattttctta ctataaaaaa gaattttcccc cagcattatt aaaacctcaa	1699
attttgatta cttgattatt attttaagta atcgcagaaa gaaagggtcgg tctatggcaa	1759
gctattttaa atccagaatc gtatcttatc tgttttattct tttggaagtg gggaccggat	1819
tcgcaatttg cgagggtgtca atggaaaatc cgaattactc ctcagcttgc gcggtcttta	1879
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cgggatactc ttaccctct tctataaaaag tgggacagac agttgaaaag ccggtaaatt	1999
catagccttg tatttcaaca gtaacttctt ctatatgcgg gtttcattttt ttcattcttg	2059
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<211> 373	
<212> PRT	

<213> Bacillus licheniformis

<400> 145

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35 40 45

Ile Val Tyr Tyr Asn Leu Leu Leu Phe Arg His Asn Leu Gln Leu Asp  
50 55 60

Tyr Met Tyr Ser Lys Pro Gly Val Asn Leu Asn Ser Arg Phe Asp Glu  
65 70 75 80

Phe Lys Lys Ile Arg Asp Gln Asn Asn Leu Glu Gly Met Leu Asp Tyr  
85 90 95

Tyr Tyr His Phe Phe Ala Gly Met Tyr His Phe Arg Gln Lys Glu Leu  
100 105 110

Ile Leu Ala Leu Asn Phe Tyr Arg Asp Ala Glu Lys Lys Leu Asp Ser  
115 120 125

Phe Asp Cys Asp Glu Leu Glu Lys Ala Glu Phe Tyr Phe Lys Ala Ser  
130 135 140

Glu Val Tyr Tyr His Met Lys Gln Thr Ile Phe Ser Met Asn Tyr Ala  
145 150 155 160

Ser Arg Ala Tyr Asn Leu Phe Lys Lys Tyr Asp Thr Tyr Gly Glu Arg  
165 170 175

Arg Val Gln Ser Gln Phe Ile Ile Ala Gly Asn Trp Leu Asp His Met  
180 185 190

Tyr Pro Glu Lys Ala Leu His Asn Leu Asn Lys Glu Leu Lys Glu Ser  
195 200 205

Glu Thr Gln Gly Ile Leu His Leu Met Gly Ser Ser His Leu Asn Ile



ctttatttta aaagggtttc gaggagctgt ggaagctgtt gcaggcatca ataaaagatc	180
aatattttct ttaagttgat cattcacaaa tcgaattact tctttatttag gccaagtttc	240
attttcatgg atgcacaggg tttatccgca aattccttca aatagtaaac ccttcaagat	300
cgcggtggac gaaattttccc ttcgagaata ctgcaggtgc ggcttgaaaa agagcatata	360
gagattcagg cgtcttagca ggcgtctttt tgttgctgat tttattgcgg cataccgaaa	420
attttttcac ttttcaacct attatcaccc gaattatagt aatatattta caaaaatgaa	480
ataaaaaggt ataggcggaa gtg aaa cag tta ata ccc tcg tca aaa gtc gga	533
Val Lys Gln Leu Ile Pro Ser Ser Lys Val Gly	
1 5 10	
gtg aaa atc cac gaa tgg tat aaa atg ata aga gag ttt agc gta ccg	581
Val Lys Ile His Glu Trp Tyr Lys Met Ile Arg Glu Phe Ser Val Pro	
15 20 25	
gat gca gag gct tta aaa gaa gaa gta gag aag gaa att aat caa atg	629
Asp Ala Glu Ala Leu Lys Glu Glu Val Glu Lys Glu Ile Asn Gln Met	
30 35 40	
gaa gaa gat cag gac tta ctc ctt tac tat cag ttg atg tgt ttt aga	677
Glu Glu Asp Gln Asp Leu Leu Leu Tyr Tyr Gln Leu Met Cys Phe Arg	
45 50 55	
cat caa tta atg tta gaa tat tta gaa cct act aac aaa aga aaa caa	725
His Gln Leu Met Leu Glu Tyr Leu Glu Pro Thr Asn Lys Arg Lys Gln	
60 65 70 75	
gga caa tca ata aac aaa ttg ttg gcc caa atc gag gag cct cga aga	773
Gly Gln Ser Ile Asn Lys Leu Leu Ala Gln Ile Glu Glu Pro Arg Arg	
80 85 90	
gat tta aat ggc ctc ctt agt tac tac tca ttt ttc ttt agg ggc atg	821
Asp Leu Asn Gly Leu Leu Ser Tyr Tyr Ser Phe Phe Phe Arg Gly Met	
95 100 105	
tat gaa ttt gag aaa aaa cag tac atc aaa gca ata gag ttt tat cga	869
Tyr Glu Phe Glu Lys Lys Gln Tyr Ile Lys Ala Ile Glu Phe Tyr Arg	
110 115 120	
aac gca gaa aaa cag ttg gct ctc att acg atg tta tagaacaagc	915
Asn Ala Glu Lys Gln Leu Ala Leu Ile Thr Met Leu	
125 130 135	
cgagtttcac tttaaaatgg ctgaagcata ctacatcatg aaacagacac atgtatcata	975
tattaagggc ctttaaaata tacaataatc atgaactcta cacagtccgt aaaatccaat	1035
gtttatttgt tatcgcggggt aactatgacg atttaatgcg ccatgacaaa gccttacccc	1095
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 tatattactc tactcaactt ctttttaagc agaaaaacta cgagcgcgca atcgagatat 1335  
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 gaatatcttg 1405

<210> 147  
 <211> 135  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 147

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Trp Tyr Lys Met Ile Arg Glu Phe Ser Val Pro Asp Ala Glu Ala Leu  
 20 25 30

Lys Glu Glu Val Glu Lys Glu Ile Asn Gln Met Glu Glu Asp Gln Asp  
 35 40 45

Leu Leu Leu Tyr Tyr Gln Leu Met Cys Phe Arg His Gln Leu Met Leu  
 50 55 60

Glu Tyr Leu Glu Pro Thr Asn Lys Arg Lys Gln Gly Gln Ser Ile Asn  
 65 70 75 80

Lys Leu Leu Ala Gln Ile Glu Glu Pro Arg Arg Asp Leu Asn Gly Leu  
 85 90 95

Leu Ser Tyr Tyr Ser Phe Phe Phe Arg Gly Met Tyr Glu Phe Glu Lys  
 100 105 110

Lys Gln Tyr Ile Lys Ala Ile Glu Phe Tyr Arg Asn Ala Glu Lys Gln  
 115 120 125

Leu Ala Leu Ile Thr Met Leu  
 130 135

<210> 148  
 <211> 2104  
 <212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1604)

<400> 148

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gtaatcgatg gtatgggtcat ttttaatgta gatttcatat tcccatccgt tttcatacgt      180
atagatcata tggcttccta caaactcttt tacatcttga ttcatatgaa ccgctccttt      240
atttgtttat tgtaatcgaa acatgtttgat atttacatat ataattataa aatgccgtca      300
aaaaagatgt caaacgaaaa tacttcctga gagatttgca caaataaaga agattgttac      360
gattaatgtc agaattttga gttatcttag gaaattatgc caatatttag aaaagtgatt      420
gtcaaaaaat aagcgattct gtaaaatgaa aaacaacca taaaaaggaa atgacatggg      480
aagaaaggaa ggataaacga ttg aag aca aaa att gcg tat gag gaa gtt gcg      533
                    Leu Lys Thr Lys Ile Ala Tyr Glu Glu Val Ala
                    1             5             10

gga atg ctt aat caa tgg tat gtc atg atc aag cgt cac gaa gta tca      581
Gly Met Leu Asn Gln Trp Tyr Val Met Ile Lys Arg His Glu Val Ser
                    15             20             25

caa gcg gtc tcg att aaa tgc gac att gag cac cag ctg ccg aat atg      629
Gln Ala Val Ser Ile Lys Cys Asp Ile Glu His Gln Leu Pro Asn Met
                    30             35             40

gaa gaa aat caa gat ctg ctt ctt tat ttt aat ctt tta gac tat cgg      677
Glu Glu Asn Gln Asp Leu Leu Leu Tyr Phe Asn Leu Leu Asp Tyr Arg
                    45             50             55

cac aag ctg ctg aca gaa gag ttt gcc gct tcc aac aaa ctg ttc gag      725
His Lys Leu Leu Thr Glu Glu Phe Ala Ala Ser Asn Lys Leu Phe Glu
                    60             65             70             75

gat att cag gag caa aaa gcc gat atg caa agc aca gat gac atg att      773
Asp Ile Gln Glu Gln Lys Ala Asp Met Gln Ser Thr Asp Asp Met Ile
                    80             85             90

gaa tat tat tat ttc ttt ttc gct ggc atg tac gaa ttt cat aag aag      821
Glu Tyr Tyr Tyr Phe Phe Phe Ala Gly Met Tyr Glu Phe His Lys Lys
                    95             100             105

gat tat aca aat gca atc aat tat tat aaa tta gcc gag gaa aag ctc      869
Asp Tyr Thr Asn Ala Ile Asn Tyr Tyr Lys Leu Ala Glu Glu Lys Leu
                    110             115             120

agg aca atc ccc gat caa atc gaa atc gcc gaa ttc cat tac aaa ctg      917
```



Arg Thr Ile Pro Asp Gln Ile Glu Ile Ala Glu Phe His Tyr Lys Leu	
125 130 135	
gct atc gcc tac tat caa atc aaa caa aat ttc ctt tcc tta aac cat	965
Ala Ile Ala Tyr Tyr Gln Ile Lys Gln Asn Phe Leu Ser Leu Asn His	
140 145 150 155	
gcg aaa aca gct cta aaa acc ttc aaa gca cat gat gat tac att caa	1013
Ala Lys Thr Ala Leu Lys Thr Phe Lys Ala His Asp Asp Tyr Ile Gln	
160 165 170	
aaa gcg atc agc aac gat atg ctg atc ggg gca aat aaa ctc gat tta	1061
Lys Ala Ile Ser Asn Asp Met Leu Ile Gly Ala Asn Lys Leu Asp Leu	
175 180 185	
ttt cgt ttt gat gaa gcc gaa cag cat tac aag caa gcc ctt aaa gac	1109
Phe Arg Phe Asp Glu Ala Glu Gln His Tyr Lys Gln Ala Leu Lys Asp	
190 195 200	
gcg gca ctg atc aaa cat cat gtc ctc ctc ggc atg gct cac cac aac	1157
Ala Ala Leu Ile Lys His His Val Leu Leu Gly Met Ala His His Asn	
205 210 215	
tta ggg ttg agc tat gtc aat cgc aac ctc ctc aca ttg gct gaa cat	1205
Leu Gly Leu Ser Tyr Val Asn Arg Asn Leu Leu Thr Leu Ala Glu His	
220 225 230 235	
cat ttc aaa gaa gcg ctg ctt atc aaa gag cat gaa gaa tcg gtt tac	1253
His Phe Lys Glu Ala Leu Leu Ile Lys Glu His Glu Glu Ser Val Tyr	
240 245 250	
ggc atc cat tcc atg ttt gaa ctg aca cat gtg ctg tac aaa tca aat	1301
Gly Ile His Ser Met Phe Glu Leu Thr His Val Leu Tyr Lys Ser Asn	
255 260 265	
gtt gtc aaa gaa gca cgc aaa ttg tat gaa aaa gga ttt ttc cgt gcg	1349
Val Val Lys Glu Ala Arg Lys Leu Tyr Glu Lys Gly Phe Phe Arg Ala	
270 275 280	
gaa aaa gca gga gaa agg gaa tat ttg tcg aaa ttt aaa ctt att cat	1397
Glu Lys Ala Gly Glu Arg Glu Tyr Leu Ser Lys Phe Lys Leu Ile His	
285 290 295	
gct ctg tat gat gaa cag gat cca ctt acg gtt gaa cat gct tta gaa	1445
Ala Leu Tyr Asp Glu Gln Asp Pro Leu Thr Val Glu His Ala Leu Glu	
300 305 310 315	
tat ctt aaa acg atc aat ctc tgg acg gat gta gcg gaa tta aca ttt	1493
Tyr Leu Lys Thr Ile Asn Leu Trp Thr Asp Val Ala Glu Leu Thr Phe	
320 325 330	
gat atc gca ctt tac tat aaa gaa aat gga gat gca gac aaa gct gcc	1541
Asp Ile Ala Leu Tyr Tyr Lys Glu Asn Gly Asp Ala Asp Lys Ala Ala	
335 340 345	
gaa tat ttt gaa gaa tct cat cat gca aga gac caa att ctt aaa aga	1589
Glu Tyr Phe Glu Glu Ser His His Ala Arg Asp Gln Ile Leu Lys Arg	

350	355	360	
acg gag gag tta aag tgaaaaaagat gattgccggtt gcgttgactg ccgtctttgc			1644
Thr Glu Glu Leu Lys			
365			
aagccttgtc gttttaagtt tttcgtctca gccgaaggga gatgccgagt ttgccggccg			1704
agccattttt cttgacgata agccggctca gctgatggcg ggcagagcga tctttctcga			1764
cagctttgac ggaaattcgc cagccgcctg acaaaacacc gcataaccct gcttgtcacc			1824
ggacaagctc tcttcgaaaa gcgccgccag cggcgctttt tttatgaaag caaatataac			1884
cggcgtccct gcaaatacgt tgcgaaagatt aaaaatatga aacacatgac aggaatggcg			1944
ctcaccggct tttggtcgaa tcctattgaa aaatctgccc gatttatagt gcttgtcatt			2004
ctataaatcc ttataatggg cttaacgccca atgtgaggca tgccaataga cagattgcag			2064
gggaaattct atactgaaca gcgcaattta gcatgtaatc			2104

<400> 149

Trp Tyr Val Met Ile Lys Arg His Glu Val Ser Gln Ala Val Ser Ile  
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Leu Leu Leu Tyr Phe Asn Leu Leu Asp Tyr Arg His Lys Leu Leu Thr  
50 55 60

Glu Glu Phe Ala Ala Ser Asn Lys Leu Phe Glu Asp Ile Gln Glu Gln  
65 70 75 80

Lys Ala Asp Met Gln Ser Thr Asp Asp Met Ile Glu Tyr Tyr Tyr Phe  
85 90 95

Phe Phe Ala Gly Met Tyr Glu Phe His Lys Lys Asp Tyr Thr Asn Ala  
100 105 110

Ile Asn Tyr Tyr Lys Leu Ala Glu Glu Lys Leu Arg Thr Ile Pro Asp  
115 120 125

Gln Ile Glu Ile Ala Glu Phe His Tyr Lys Leu Ala Ile Ala Tyr Tyr  
130 135 140

Gln Ile Lys Gln Asn Phe Leu Ser Leu Asn His Ala Lys Thr Ala Leu  
145 150 155 160

Lys Thr Phe Lys Ala His Asp Asp Tyr Ile Gln Lys Ala Ile Ser Asn  
165 170 175

Asp Met Leu Ile Gly Ala Asn Lys Leu Asp Leu Phe Arg Phe Asp Glu  
180 185 190

Ala Glu Gln His Tyr Lys Gln Ala Leu Lys Asp Ala Ala Leu Ile Lys  
195 200 205

His His Val Leu Leu Gly Met Ala His His Asn Leu Gly Leu Ser Tyr  
210 215 220

Val Asn Arg Asn Leu Leu Thr Leu Ala Glu His His Phe Lys Glu Ala  
225 230 235 240

Leu Leu Ile Lys Glu His Glu Glu Ser Val Tyr Gly Ile His Ser Met  
245 250 255

Phe Glu Leu Thr His Val Leu Tyr Lys Ser Asn Val Val Lys Glu Ala  
260 265 270

Arg Lys Leu Tyr Glu Lys Gly Phe Phe Arg Ala Glu Lys Ala Gly Glu  
275 280 285

Arg Glu Tyr Leu Ser Lys Phe Lys Leu Ile His Ala Leu Tyr Asp Glu  
290 295 300

Gln Asp Pro Leu Thr Val Glu His Ala Leu Glu Tyr Leu Lys Thr Ile  
305 310 315 320

Asn Leu Trp Thr Asp Val Ala Glu Leu Thr Phe Asp Ile Ala Leu Tyr  
325 330 335

Tyr Lys Glu Asn Gly Asp Ala Asp Lys Ala Ala Glu Tyr Phe Glu Glu  
340 345 350

Ser His His Ala Arg Asp Gln Ile Leu Lys Arg Thr Glu Glu Leu Lys  
355 360 365

<210> 150  
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<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(881)

<400> 150  
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aagtcggagt gaaaatccac gaatggtata aaatgataag agagtttagc gtaccggatg 120  
cagaggcttt aaaagaagaa gtagagaagg aaattaatca aatggaagaa gatcaggact 180  
tactccttta ctatcagttg atgtgtttta gacatcaatt aatgttagaa tatttagaac 240  
ctactaacia aagaaaacia ggacaatcaa taaacaaatt gttggcccaa atcgaggagc 300  
ctcgaagaga tttaaattggc ctccttagtt actactcatt tttctttagg ggcatgtatg 360  
aatattgagaa aaaacagtac atcaaagcaa tagagtttta tcgaaacgca gaaaaacagt 420  
tggctctcat tacgatgtta tagaacaagc cgagtttcac tttaaaatgg ctgaagcata 480  
ctacatcatg aaacagacac atg tat cat ata tta agg gcc ttt aaa ata tac 533  
Met Tyr His Ile Leu Arg Ala Phe Lys Ile Tyr  
1 5 10  
aat aat cat gaa ctc tac aca gtc cgt aaa atc caa tgt tta ttt gtt 581  
Asn Asn His Glu Leu Tyr Thr Val Arg Lys Ile Gln Cys Leu Phe Val  
15 20 25  
atc gcg ggt aac tat gac gat tta atg cgc cat gac aaa gcc tta ccc 629  
Ile Ala Gly Asn Tyr Asp Asp Leu Met Arg His Asp Lys Ala Leu Pro  
30 35 40  
cac ctg gaa aat gca ctt gaa tta gcg ata gag atc gac aat aaa agg 677  
His Leu Glu Asn Ala Leu Glu Leu Ala Ile Glu Ile Asp Asn Lys Arg  
45 50 55  
ctc att agt tct gcc tat ttt aat ata gcc gac tgt cat gaa tgt atg 725  
Leu Ile Ser Ser Ala Tyr Phe Asn Ile Ala Asp Cys His Glu Cys Met  
60 65 70 75  
gga gac att gat gca gca gtt gaa tat gct gaa aaa gcc gta gag att 773  
Gly Asp Ile Asp Ala Ala Val Glu Tyr Ala Glu Lys Ala Val Glu Ile

80	85	90	
aat cta aaa gaa gaa tat aac aac cta cca caa tca tta tat tac tct			821
Asn Leu Lys Glu Glu Tyr Asn Asn Leu Pro Gln Ser Leu Tyr Tyr Ser			
95	100	105	
act caa ctt ctt ttt aag cag aaa aac tac gag cgc gca atc gag ata			869
Thr Gln Leu Leu Phe Lys Gln Lys Asn Tyr Glu Arg Ala Ile Glu Ile			
110	115	120	
ttt ctt att ggt tagacaaaca gctcgaaaat tcaacgatac cctattcact			921
Phe Leu Ile Gly			
125			
tctctatttg aatatcttga ggcgttatat atctattctg tgaataaaaga agagatttta			981
gaggatattta aataacttga ggagaataaa atatttgcac acatagaaga gctttcgctt			1041
gaagtctcta accaataacct tgaaagaaaa gaccatagaa actcaatcga gttccttcaa			1101
aaaatgatgt atgggcaaac aaaaattaaa aaaggggagt gtctctatga gtattaaaaa			1161
gctcgttatt cccatttttag cgcgcgcgtt attaacgatg ggtatttagcg ttgtttcagc			1221
aaccgaccag tctgacggcg tatatcaaat cgctacccgt aagcaaacgt aagaaacgcc			1281
ccaaatgtgg ggcgcttttt atttctacgg tttcttaacg ttaaaccatcg tgattaactt			1341
cttatcagct gtcggttaaga ttaacgtata ccattccgac			1381

<210> 151  
 <211> 127  
 <212> PRT  
 <213> *Bacillus licheniformis*

<400> 151

Met Tyr His Ile Leu Arg Ala Phe Lys Ile Tyr Asn Asn His Glu Leu
1 5 10 15

Tyr Thr Val Arg Lys Ile Gln Cys Leu Phe Val Ile Ala Gly Asn Tyr
20 25 30

Asp Asp Leu Met Arg His Asp Lys Ala Leu Pro His Leu Glu Asn Ala
35 40 45

Leu Glu Leu Ala Ile Glu Ile Asp Asn Lys Arg Leu Ile Ser Ser Ala
50 55 60

Tyr Phe Asn Ile Ala Asp Cys His Glu Cys Met Gly Asp Ile Asp Ala
65 70 75 80

Ala Val Glu Tyr Ala Glu Lys Ala Val Glu Ile Asn Leu Lys Glu Glu  
85 90 95

Tyr Asn Asn Leu Pro Gln Ser Leu Tyr Tyr Ser Thr Gln Leu Leu Phe  
100 105 110

Lys Gln Lys Asn Tyr Glu Arg Ala Ile Glu Ile Phe Leu Ile Gly  
115 120 125

<210> 152  
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<212> DNA  
<213> Bacillus licheniformis

<220>  
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ccaaagaatt gatttggagc gggaaaaaat tgacgggggc cgaagcgcac gagcttcgga 120  
tcgcagacgc cgtattcagc ggggactccg gccgttttgc gcgcatttat cttgaaaagc 180  
ttctgcacgc tccgctggca gcgatgattg agacaaaaaa gatctatcag gcgttgaatg 240  
gaggcaggct gcagaaaacg cttgaactcg agaaaacggc ccagatgaaa atgaggctga 300  
caagcgacca tcaggaaggg atccgcgcac ttttagaaaa gcgccagccg caatttaacc 360  
gtcagcaagt ataacaagag cgggccggca ggaaattgac cttgggaaat gatgtgcaga 420  
aacaattgta aaaaaattta agtttccata aaatgattca taagatacag atctgtacga 480  
agtccttggga ggcggcgaaa ttg aaa cag aag att cca tct gaa tac gtt gct 533  
Leu Lys Gln Lys Ile Pro Ser Glu Tyr Val Ala  
1 5 10  
aga aag ctg aat gat tgg tac aac gcc att cgg aaa aat cag atc gcc 581  
Arg Lys Leu Asn Asp Trp Tyr Asn Ala Ile Arg Lys Asn Gln Ile Ala  
15 20 25  
gcc agt gaa tca ttg aaa gcg gaa att tta aat gat ttt caa gac atg 629  
Ala Ser Glu Ser Leu Lys Ala Glu Ile Leu Asn Asp Phe Gln Asp Met  
30 35 40  
gaa gaa aat cgg gac gtc ctg ctc tac tat tcg ctg ctt gaa ttc agg 677  
Glu Glu Asn Arg Asp Val Leu Leu Tyr Tyr Ser Leu Leu Glu Phe Arg  
45 50 55  
cat aaa ctg atg ctc agc tat ttg aaa ccg aaa gag act gaa aat att 725

His Lys Leu Met Leu Ser Tyr Leu Lys Pro Lys Glu Thr Glu Asn Ile	
60 65 70 75	
gaa aaa aac ctc cgc gac tta gaa gaa aaa gaa gac caa atg acg ggt	773
Glu Lys Asn Leu Arg Asp Leu Glu Glu Lys Glu Asp Gln Met Thr Gly	
80 85 90	
tta tta aac tat tat tac tgg ttt ttt aaa ggg atg tat gag ttc aaa	821
Leu Leu Asn Tyr Tyr Tyr Trp Phe Phe Lys Gly Met Tyr Glu Phe Lys	
95 100 105	
caa aag cgg ttc gtc aaa gca atc ggc tgc tat aaa acg gct gaa caa	869
Gln Lys Arg Phe Val Lys Ala Ile Gly Cys Tyr Lys Thr Ala Glu Gln	
110 115 120	
aaa gtc agc gca ctg gaa gac gag gtt gaa aaa gcg gaa ttt tat tat	917
Lys Val Ser Ala Leu Glu Asp Glu Val Glu Lys Ala Glu Phe Tyr Tyr	
125 130 135	
aag ctt gcg gaa atc tac tat tat atc aac cag aga tac ctg tcg atc	965
Lys Leu Ala Glu Ile Tyr Tyr Tyr Ile Asn Gln Arg Tyr Leu Ser Ile	
140 145 150 155	
aac tat gcg acg cta gct tcc gac att ttt aac cgg tat gaa acg cta	1013
Asn Tyr Ala Thr Leu Ala Ser Asp Ile Phe Asn Arg Tyr Glu Thr Leu	
160 165 170	
aaa gaa aaa aag att ttc tgc gat ttt atc att gcc ggt aat tgg gtt	1061
Lys Glu Lys Lys Ile Phe Cys Asp Phe Ile Ile Ala Gly Asn Trp Val	
175 180 185	
gaa tcg atg aca tac gga ccc gcg ctg aaa agc ctg gcc aat gcg ctt	1109
Glu Ser Met Thr Tyr Gly Pro Ala Leu Lys Ser Leu Ala Asn Ala Leu	
190 195 200	
gaa gac gcc agg aaa atc aaa aac agc cat ttg acg gca gcc gct cat	1157
Glu Asp Ala Arg Lys Ile Lys Asn Ser His Leu Thr Ala Ala Ala His	
205 210 215	
ttt aat ttg gga aat tgc tat ttc cac caa gaa tcg tac cgg gaa gcc	1205
Phe Asn Leu Gly Asn Cys Tyr Phe His Gln Glu Ser Tyr Arg Glu Ala	
220 225 230 235	
tca gat cat atg gag cgc cct ttc cat ttt tgaacaggaa agttcatcat	1255
Ser Asp His Met Glu Arg Pro Phe His Phe	
240 245	
atattcccaa agtgctgtac aacttgatgt acgtccgtct caagcagggg aaccatgccg	1315
gagctgccgc ctgttatgaa aaaggcatcc gaagcgcggc atcgctcggg gatgaagaac	1375
acgcggcaaaa gcttaacatt ctgtgcgggc tgtatttaga cggaggggat cagaaagccg	1435
tggaaaacgg atttgattat ttggagtcaa atcatttata tgctgctgtt gaagagctgg	1495
ctttagatgc agcccagtat tataatcaaa ttgagcggct gaaagattcc attttttact	1555

atgaaaagtg cgctcaggca agtcgaaaaa tcaaaagggg agatgcgttg tatgaaagct 1615  
aaactgttgt tcgtcgcggt gtcgctggct gttgtgttaa cgtcttcaag ctttttggca 1675  
gatgcgggga aagccccttc cttgtatgcg gacaaaatga tcacgactga caaggaggct 1735

<210> 153  
<211> 245  
<212> PRT  
<213> Bacillus licheniformis

<400> 153

Leu Lys Gln Lys Ile Pro Ser Glu Tyr Val Ala Arg Lys Leu Asn Asp  
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Trp Tyr Asn Ala Ile Arg Lys Asn Gln Ile Ala Ala Ser Glu Ser Leu  
20 25 30

Lys Ala Glu Ile Leu Asn Asp Phe Gln Asp Met Glu Glu Asn Arg Asp  
35 40 45

Val Leu Leu Tyr Tyr Ser Leu Leu Glu Phe Arg His Lys Leu Met Leu  
50 55 60

Ser Tyr Leu Lys Pro Lys Glu Thr Glu Asn Ile Glu Lys Asn Leu Arg  
65 70 75 80

Asp Leu Glu Glu Lys Glu Asp Gln Met Thr Gly Leu Leu Asn Tyr Tyr  
85 90 95

Tyr Trp Phe Phe Lys Gly Met Tyr Glu Phe Lys Gln Lys Arg Phe Val  
100 105 110

Lys Ala Ile Gly Cys Tyr Lys Thr Ala Glu Gln Lys Val Ser Ala Leu  
115 120 125

Glu Asp Glu Val Glu Lys Ala Glu Phe Tyr Tyr Lys Leu Ala Glu Ile  
130 135 140

Tyr Tyr Tyr Ile Asn Gln Arg Tyr Leu Ser Ile Asn Tyr Ala Thr Leu  
145 150 155 160

Ala Ser Asp Ile Phe Asn Arg Tyr Glu Thr Leu Lys Glu Lys Lys Ile  
165 170 175



Phe Cys Asp Phe Ile Ile Ala Gly Asn Trp Val Glu Ser Met Thr Tyr  
 180 185 190

Gly Pro Ala Leu Lys Ser Leu Ala Asn Ala Leu Glu Asp Ala Arg Lys  
 195 200 205

Ile Lys Asn Ser His Leu Thr Ala Ala Ala His Phe Asn Leu Gly Asn  
 210 215 220

Cys Tyr Phe His Gln Glu Ser Tyr Arg Glu Ala Ser Asp His Met Glu  
 225 230 235 240

Arg Pro Phe His Phe  
 245

<210> 154  
 <211> 2116  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
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 <222> (501)..(1616)

<400> 154  
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 gttccagcgt ttgatctatt gcattgtgca ggcctgaac atcaagagtc ttcattggcat 180  
 tctcctctaa tccttttcat tacaatcagt atatagttta ccactttata gaaagtactt 240  
 ggtgaatata tcctgttcaa ccatgaaaat gaatcattgg gcttaggtca ttatttctat 300  
 tgattcattt cgattaccgt aaacaagttt gttgtagcat tctttaggct ctgtgactaa 360  
 accaaaaagc catttgtttt aaattggtct ttcggtatca cgaaaatttc gttttttggg 420  
 ctgatagaag ttttgcaatt atgaattgta tgtaaatctt taacataaaa aggatggttag 480  
 ctggaaggga atgatggcag ttg gag act atc ccg tct tca gaa gtt gga atc 533  
 Leu Glu Thr Ile Pro Ser Ser Glu Val Gly Ile  
 1 5 10  
 aaa ata aac cgc tgg tac aac gaa att caa aaa tta aac gta ata gaa 581  
 Lys Ile Asn Arg Trp Tyr Asn Glu Ile Gln Lys Leu Asn Val Ile Glu  
 15 20 25  
 gca gaa cga tta aag gcg gaa gtt cac tta gct ata gaa aga atg gaa 629

Ala	Glu	Arg	Leu	Lys	Ala	Glu	Val	His	Leu	Ala	Ile	Glu	Arg	Met	Glu		
		30					35					40					
gaa	gat	cag	gac	ttg	ctt	tcc	tat	tat	cag	ctt	atg	aat	ttt	aga	cat	677	
Glu	Asp	Gln	Asp	Leu	Leu	Ser	Tyr	Tyr	Gln	Leu	Met	Asn	Phe	Arg	His		
	45					50					55						
gag	tta	atg	ttg	gaa	tat	ctt	ttc	ccg	gca	gaa	aaa	aag	ctg	agc	aaa	725	
Glu	Leu	Met	Leu	Glu	Tyr	Leu	Phe	Pro	Ala	Glu	Lys	Lys	Leu	Ser	Lys		
	60				65				70						75		
tct	gat	tat	ctt	agg	gaa	att	gag	gga	cag	gga	aga	aaa	ttg	tca	ggc	773	
Ser	Asp	Tyr	Leu	Arg	Glu	Ile	Glu	Gly	Gln	Gly	Arg	Lys	Leu	Ser	Gly		
				80					85					90			
ttg	ctc	gaa	tac	tat	ttt	tcc	ttt	ttc	acc	gga	atg	tat	cat	ttt	tct	821	
Leu	Leu	Glu	Tyr	Tyr	Phe	Ser	Phe	Phe	Thr	Gly	Met	Tyr	His	Phe	Ser		
			95					100					105				
cgc	gga	aaa	tac	ata	aag	gca	atc	aag	gca	tat	aga	gca	gca	gaa	aaa	869	
Arg	Gly	Lys	Tyr	Ile	Lys	Ala	Ile	Lys	Ala	Tyr	Arg	Ala	Ala	Glu	Lys		
		110					115					120					
aag	ttg	acg	aaa	gtt	tca	gat	aaa	ata	gaa	aag	gct	gaa	ttc	tat	tat	917	
Lys	Leu	Thr	Lys	Val	Ser	Asp	Lys	Ile	Glu	Lys	Ala	Glu	Phe	Tyr	Tyr		
	125					130					135						
aag	atg	gcg	gaa	gtg	ttt	tat	cat	atg	aaa	cag	act	cat	atg	tca	atg	965	
Lys	Met	Ala	Glu	Val	Phe	Tyr	His	Met	Lys	Gln	Thr	His	Met	Ser	Met		
	140				145					150					155		
tat	tat	gtg	tct	ctc	gct	tat	gat	att	tat	aaa	tcc	tat	gat	gca	tat	1013	
Tyr	Tyr	Val	Ser	Leu	Ala	Tyr	Asp	Ile	Tyr	Lys	Ser	Tyr	Asp	Ala	Tyr		
				160					165					170			
gtg	att	cga	aga	att	aat	tgt	cta	ttc	gtt	gtt	gct	ggg	aat	tac	att	1061	
Val	Ile	Arg	Arg	Ile	Asn	Cys	Leu	Phe	Val	Val	Ala	Gly	Asn	Tyr	Ile		
			175					180					185				
gat	tta	tca	acc	cat	gat	caa	gct	tta	ccg	cat	ctt	tta	agc	gct	aag	1109	
Asp	Leu	Ser	Thr	His	Asp	Gln	Ala	Leu	Pro	His	Leu	Leu	Ser	Ala	Lys		
		190					195					200					
gaa	tcc	gcg	gaa	gac	att	caa	aac	aag	gcg	atc	gtt	gca	aag	gct	ctt	1157	
Glu	Ser	Ala	Glu	Asp	Ile	Gln	Asn	Lys	Ala	Ile	Val	Ala	Lys	Ala	Leu		
	205					210					215						
tta	aat	gta	gca	tat	tgt	tat	aat	gca	atg	gag	aga	cca	aca	aaa	gct	1205	
Leu	Asn	Val	Ala	Tyr	Cys	Tyr	Asn	Ala	Met	Glu	Arg	Pro	Thr	Lys	Ala		
	220				225					230					235		
att	gaa	tac	ttt	cat	aag	gcg	att	gat	gta	gca	aag	gaa	ata	aag	gca	1253	
Ile	Glu	Tyr	Phe	His	Lys	Ala	Ile	Asp	Val	Ala	Lys	Glu	Ile	Lys	Ala		
				240					245					250			
aaa	gaa	ctg	act	cag	gct	tat	tat	gat	ttg	gca	tta	att	cac	ttt	cga	1301	
Lys	Glu	Leu	Thr	Gln	Ala	Tyr	Tyr	Asp	Leu	Ala	Leu	Ile	His	Phe	Arg		

255	260	265	
aat aac gaa aat att gaa gga cga aaa ttt tat gaa aag gcg ctt gaa			1349
Asn Asn Glu Asn Ile Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu			
270	275	280	
agt gcg cgg gta ttt gaa gat gaa tta ttc ctg tgt ctg ttg gat gtt			1397
Ser Ala Arg Val Phe Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val			
285	290	295	
tta gag gca ctg ttt ata aaa tca gct aat aag tca gag gta cta gaa			1445
Leu Glu Ala Leu Phe Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu			
300	305	310	315
aca atg aaa cca tta cgg gat agt cgt ggt tac ccc tat ctt gag gaa			1493
Thr Met Lys Pro Leu Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu			
320	325	330	
ctg gca tta gaa gca gct cta ttc tat act agg aat gag cgg cca aat			1541
Leu Ala Leu Glu Ala Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn			
335	340	345	
gat tcc ata ttt ttt tat gat cag atg gtg cag gct cag aaa caa atc			1589
Asp Ser Ile Phe Phe Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile			
350	355	360	
aaa agg ggc gac ttt ctg tat gaa atc taagctgttt ctttcgctga			1636
Lys Arg Gly Asp Phe Leu Tyr Glu Ile			
365	370		
cccttgcttt gggcttggtg gtcgtgtcga gcgcttccat tcacacatct gttgaacaac			1696
aacatgcaga attttctgta gcatctaggc tcgcaacata attgtgtttg ggcaggtcat			1756
gtgatggcct gccttttttg tgaaagaatt attttagttt gaaaaccaga acgattgtgt			1816
taatactcat ctttcttcgt cccttggtgtt ggaattttca tcatatcaat atttgaatat			1876
gcggctgtcc gcattattaa caattttaaa tttttgcac aaattttata caaaggcaga			1936
caaaaacctt gatatatcaa tggttctatg ggtatattca accacgacca ccgatatcgc			1996
taaaaaccgt attgccaaac gacgaaagag cgttccttac acaaggaatg ctctttttgt			2056
ttattcctca tcaaagcgga gagccgcaa cataaacgca atgaccaact gttgtccgca			2116
<210> 155			
<211> 372			
<212> PRT			
<213> Bacillus licheniformis			
<400> 155			
Leu Glu Thr Ile Pro Ser Ser Glu Val Gly Ile Lys Ile Asn Arg Trp			
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Tyr Asn Glu Ile Gln Lys Leu Asn Val Ile Glu Ala Glu Arg Leu Lys  
 20 25 30

Ala Glu Val His Leu Ala Ile Glu Arg Met Glu Glu Asp Gln Asp Leu  
 35 40 45

Leu Ser Tyr Tyr Gln Leu Met Asn Phe Arg His Glu Leu Met Leu Glu  
 50 55 60

Tyr Leu Phe Pro Ala Glu Lys Lys Leu Ser Lys Ser Asp Tyr Leu Arg  
 65 70 75 80

Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly Leu Leu Glu Tyr Tyr  
 85 90 95

Phe Ser Phe Phe Thr Gly Met Tyr His Phe Ser Arg Gly Lys Tyr Ile  
 100 105 110

Lys Ala Ile Lys Ala Tyr Arg Ala Ala Glu Lys Lys Leu Thr Lys Val  
 115 120 125

Ser Asp Lys Ile Glu Lys Ala Glu Phe Tyr Tyr Lys Met Ala Glu Val  
 130 135 140

Phe Tyr His Met Lys Gln Thr His Met Ser Met Tyr Tyr Val Ser Leu  
 145 150 155 160

Ala Tyr Asp Ile Tyr Lys Ser Tyr Asp Ala Tyr Val Ile Arg Arg Ile  
 165 170 175

Asn Cys Leu Phe Val Val Ala Gly Asn Tyr Ile Asp Leu Ser Thr His  
 180 185 190

Asp Gln Ala Leu Pro His Leu Leu Ser Ala Lys Glu Ser Ala Glu Asp  
 195 200 205

Ile Gln Asn Lys Ala Ile Val Ala Lys Ala Leu Leu Asn Val Ala Tyr  
 210 215 220

Cys Tyr Asn Ala Met Glu Arg Pro Thr Lys Ala Ile Glu Tyr Phe His  
 225 230 235 240

Lys Ala Ile Asp Val Ala Lys Glu Ile Lys Ala Lys Glu Leu Thr Gln  
 245 250 255

Ala Tyr Tyr Asp Leu Ala Leu Ile His Phe Arg Asn Asn Glu Asn Ile  
 260 265 270

Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu Ser Ala Arg Val Phe  
 275 280 285

Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val Leu Glu Ala Leu Phe  
 290 295 300

Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu Thr Met Lys Pro Leu  
 305 310 315 320

Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu Leu Ala Leu Glu Ala  
 325 330 335

Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn Asp Ser Ile Phe Phe  
 340 345 350

Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile Lys Arg Gly Asp Phe  
 355 360 365

Leu Tyr Glu Ile  
 370

<210> 156  
 <211> 1576  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1268)

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 caagcttcac aaaaccggtc gatgccggag aaatcgaaga aaagctggac acttcacacg 180  
 gcatgattcg gactgaggtg agaagcaagt ctgccgattc ccatcttgga cacgtgtttc 240  
 cggacggacc cggaccggac ggcttgcgct attgcatcaa ttcagccgcc ctccggtttg 300

tgccgaagga cgaccttgag aaagaaggat acggcggaata tgtcaaactg tttgaacgca	360
agaaatccgg agaggaaagc tgaggagagc agcatgcaag atgatccttt tttcaaaggg	420
tcattcttttt ttagaggatt ttctgctctg aaagcgaaaa aacattacaa tagatcatct	480
tgagaaaaaga ggcagccggt gtg aca tcc att tca aac aca gaa gac cgt tat	533
Val Thr Ser Ile Ser Asn Thr Glu Asp Arg Tyr	
1 5 10	
tta atg ctg aca tgc agc aaa aaa att gaa tcc cat tat cat ata tac	581
Leu Met Leu Thr Cys Ser Lys Lys Ile Glu Ser His Tyr His Ile Tyr	
15 20 25	
aca gat gag gag atc ccg cag atg ttt tcc tct cat ttt ctg cag ctg	629
Thr Asp Glu Glu Ile Pro Gln Met Phe Ser Ser His Phe Leu Gln Leu	
30 35 40	
cag gac gat ttt ccg ctg aca gag ctg tac tcc ctg ctc gtt cgg aca	677
Gln Asp Asp Phe Pro Leu Thr Glu Leu Tyr Ser Leu Leu Val Arg Thr	
45 50 55	
ccc gaa att tta aaa cga aat tat gtt cat gtg aaa agc tct tat aag	725
Pro Glu Ile Leu Lys Arg Asn Tyr Val His Val Lys Ser Ser Tyr Lys	
60 65 70 75	
cgg gat ctg cct ttt acg atg aaa aag tcg ctc ttt gat ctt ggc tat	773
Arg Asp Leu Pro Phe Thr Met Lys Lys Ser Leu Phe Asp Leu Gly Tyr	
80 85 90	
att ctt gat gaa gaa ttg ttt tat tcc atc agg ctt gca gat tgg aaa	821
Ile Leu Asp Glu Glu Leu Phe Tyr Ser Ile Arg Leu Ala Asp Trp Lys	
95 100 105	
gga gat tcc cct ggt gta cgg gca gag tgg ggg acg gag aaa tcg ctc	869
Gly Asp Ser Pro Gly Val Arg Ala Glu Trp Gly Thr Glu Lys Ser Leu	
110 115 120	
att gac ggc tgc cgc atg atg cag gct tat gat aca ttg tct atc aat	917
Ile Asp Gly Cys Arg Met Met Gln Ala Tyr Asp Thr Leu Ser Ile Asn	
125 130 135	
gaa gcg ttt gcg aag gaa aag ctg ctg cgc aag tat cct ttt tat gag	965
Glu Ala Phe Ala Lys Glu Lys Leu Leu Arg Lys Tyr Pro Phe Tyr Glu	
140 145 150 155	
gaa ggc atc att cag ctg tgt gtc tgc tac tcg gaa gaa ggc gaa ccg	1013
Glu Gly Ile Ile Gln Leu Cys Val Cys Tyr Ser Glu Glu Gly Glu Pro	
160 165 170	
att gga tgt gct gag ctt tat ctc gat cac gac gaa aac gtt gct aaa	1061
Ile Gly Cys Ala Glu Leu Tyr Leu Asp His Asp Glu Asn Val Ala Lys	
175 180 185	
atc gaa gaa gtc gcc att ttg gag cca tac cag cgg aaa ggc tat gga	1109
Ile Glu Glu Val Ala Ile Leu Glu Pro Tyr Gln Arg Lys Gly Tyr Gly	
190 195 200	

tcg ggc ctt atc aag cag atg ctc acc gcc gcc aaa caa tcg ggc atg	1157
Ser Gly Leu Ile Lys Gln Met Leu Thr Ala Ala Lys Gln Ser Gly Met	
205 210 215	
gaa tcg tgc tat ctt gta act tcg gga agc gat cag gtg aaa acg ttt	1205
Glu Ser Cys Tyr Leu Val Thr Ser Gly Ser Asp Gln Val Lys Thr Phe	
220 225 230 235	
tat gaa aag ctg ggc ttt cag cag aag gaa aag ctc acg aca ata ttt	1253
Tyr Glu Lys Leu Gly Phe Gln Gln Lys Glu Lys Leu Thr Thr Ile Phe	
240 245 250	
aaa tat ttg ttc gta taaagtaggc aggtgcacat accaattggg acttggcctg	1308
Lys Tyr Leu Phe Val	
255	
cataggctgg ggtgtagact ttatacgaaa ggatgataag cctgtgcatt actcccatta	1368
ttgctgtcct actggaggat acggctacgg gtttcacgga agaacacatt tgactcatcg	1428
ttgtcctctt tattttgctc atcattgtcg gtgcggcttt catttgctag ctaaaagccc	1488
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ttggaaaatt ttgcattcgt atgtaata	1576

<210> 157  
 <211> 256  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 157

Val Thr Ser Ile Ser Asn Thr Glu Asp Arg Tyr Leu Met Leu Thr Cys
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Ser Lys Lys Ile Glu Ser His Tyr His Ile Tyr Thr Asp Glu Glu Ile
20 25 30

Pro Gln Met Phe Ser Ser His Phe Leu Gln Leu Gln Asp Asp Phe Pro
35 40 45

Leu Thr Glu Leu Tyr Ser Leu Leu Val Arg Thr Pro Glu Ile Leu Lys
50 55 60

Arg Asn Tyr Val His Val Lys Ser Ser Tyr Lys Arg Asp Leu Pro Phe
65 70 75 80

Thr Met Lys Lys Ser Leu Phe Asp Leu Gly Tyr Ile Leu Asp Glu Glu
85 90 95

Leu Phe Tyr Ser Ile Arg Leu Ala Asp Trp Lys Gly Asp Ser Pro Gly  
100 105 110

Val Arg Ala Glu Trp Gly Thr Glu Lys Ser Leu Ile Asp Gly Cys Arg  
115 120 125

Met Met Gln Ala Tyr Asp Thr Leu Ser Ile Asn Glu Ala Phe Ala Lys  
130 135 140

Glu Lys Leu Leu Arg Lys Tyr Pro Phe Tyr Glu Glu Gly Ile Ile Gln  
145 150 155 160

Leu Cys Val Cys Tyr Ser Glu Glu Gly Glu Pro Ile Gly Cys Ala Glu  
165 170 175

Leu Tyr Leu Asp His Asp Glu Asn Val Ala Lys Ile Glu Glu Val Ala  
180 185 190

Ile Leu Glu Pro Tyr Gln Arg Lys Gly Tyr Gly Ser Gly Leu Ile Lys  
195 200 205

Gln Met Leu Thr Ala Ala Lys Gln Ser Gly Met Glu Ser Cys Tyr Leu  
210 215 220

Val Thr Ser Gly Ser Asp Gln Val Lys Thr Phe Tyr Glu Lys Leu Gly  
225 230 235 240

Phe Gln Gln Lys Glu Lys Leu Thr Thr Ile Phe Lys Tyr Leu Phe Val  
245 250 255

<210> 158  
<211> 1783  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(1283)

<400> 158  
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ttattgacaa acgcaaacga tttttttcgt cccggcccg c agtaagactg gcagccgatt	180
tccacttttg catccggatc aattttctttc agacggggca aaagcgtctt taaattgggtg	240
gcctggcaat cgtcgcatac tcgaaattca ttagccattt catacgcttc ctttcgtttt	300
gttcatctgt ctttatgaaa ggcattcaac tgtgccgaac ttttataaaa aatgacacca	360
tccttcattt tacaaggatt ctttcattcc tgcaaggatc gcgctaaaaa aatcagttcc	420
tattctttta gcaaacttgt ataaatatatt tccaaaatgg acaatctaata accaatactg	480
acaatgggag ttgagaagtg atg aaa caa aga caa gac gct tgg tct gag gaa	533
Met Lys Gln Arg Gln Asp Ala Trp Ser Glu Glu	
1 5 10	
aat gat tta ctg ctt gct gaa acg gta ttg cgg cat gtc agg gaa ggg	581
Asn Asp Leu Leu Leu Ala Glu Thr Val Leu Arg His Val Arg Glu Gly	
15 20 25	
agc aca cag ctg aac gcc ttc gag gaa gtc gga gac aga ctg aac agg	629
Ser Thr Gln Leu Asn Ala Phe Glu Glu Val Gly Asp Arg Leu Asn Arg	
30 35 40	
aca tca gcc gcc tgc ggt ttt aga tgg aac gca gtt gtc cgc cac caa	677
Thr Ser Ala Ala Cys Gly Phe Arg Trp Asn Ala Val Val Arg His Gln	
45 50 55	
tac gaa aaa gca ttg cag ctg gct aaa aaa cag agg aag caa aga atg	725
Tyr Glu Lys Ala Leu Gln Leu Ala Lys Lys Gln Arg Lys Gln Arg Met	
60 65 70 75	
cgc gcc ctc gga aac gga cag ccg gcg aaa aaa cgc tta tta tac aag	773
Arg Ala Leu Gly Asn Gly Gln Pro Ala Lys Lys Arg Leu Leu Tyr Lys	
80 85 90	
ccg ccg gtc gaa acg aat gct gaa cct cct gca gaa agc gtt gtt gag	821
Pro Pro Val Glu Thr Asn Ala Glu Pro Pro Ala Glu Ser Val Val Glu	
95 100 105	
cag aag aaa gca acc gca gat tca agc gaa cag cag ccg atc gcc agc	869
Gln Lys Lys Ala Thr Ala Asp Ser Ser Glu Gln Gln Pro Ile Ala Ser	
110 115 120	
gag cat ctg cct tat gtt gat gag agc ttt aaa gaa gag tta gct agt	917
Glu His Leu Pro Tyr Val Asp Glu Ser Phe Lys Glu Glu Leu Ala Ser	
125 130 135	
tta tct cac ctt cta tcg cca aat cag ccg cag gcc ggc cat aca gcc	965
Leu Ser His Leu Leu Ser Pro Asn Gln Pro Gln Ala Gly His Thr Ala	
140 145 150 155	
gat aca tcg aaa gac atg acg atc gat gat gtg atc cgc ttc ctg caa	1013
Asp Thr Ser Lys Asp Met Thr Ile Asp Asp Val Ile Arg Phe Leu Gln	
160 165 170	
aac tat aca gga aac gaa gaa caa act gcc gct tta aaa atg gaa aat	1061

Asn Tyr Thr Gly Asn Glu Glu Gln Thr Ala Ala Leu Lys Met Glu Asn	
175 180 185	
gaa cgt tta aaa cag gaa aac gaa gaa ctg acg aag aaa gtt gaa aag	1109
Glu Arg Leu Lys Gln Glu Asn Glu Glu Leu Thr Lys Lys Val Glu Lys	
190 195 200	
ctt gaa gcg gaa gtc aaa aag ctg gaa aaa gac cag aca acc atc cag	1157
Leu Glu Ala Glu Val Lys Lys Leu Glu Lys Asp Gln Thr Thr Ile Gln	
205 210 215	
gaa gac tac gaa acg ctc gta aaa att atg aac cgt gca aga aaa cta	1205
Glu Asp Tyr Glu Thr Leu Val Lys Ile Met Asn Arg Ala Arg Lys Leu	
220 225 230 235	
gtt tta ttc gaa gaa gac gaa cac gct gcg ccc gcc ttc aaa atg gac	1253
Val Leu Phe Glu Glu Asp Glu His Ala Ala Pro Ala Phe Lys Met Asp	
240 245 250	
cgg aac ggc aat tta gaa aaa atg gct gaa tagcgctctc agaggatgcg	1303
Arg Asn Gly Asn Leu Glu Lys Met Ala Glu	
255 260	
gcagagacgt tcaggcagca aggactgaca atgcatacaa acattttttcg atacgaggat	1363
accccttttct ttaaaaaagg gggatattttt accttttctgc ggcttgcttt tatatgacaa	1423
aaatttcata atagggatag caattcataa ggcgggggtat tcgatgaagt ttgttttata	1483
tgcggttcag ttcggcactg cggccctttt gtttttgctt tctgcattgg caagctggta	1543
tcaaggcagc gagcttttaa aggtgccgtg ggagtggaaa tatacagcca agtttacaag	1603
ttggctgtac ggagaggact ccattaaaaa cgcacataat atttcacagc ttgatttttt	1663
cgtctatgcg gccaaagcata cgccggcaac cgttatttta atggccgtca gtttggcgta	1723
tatcatcgct ttggcggctt atcttctcat caaaacatat gtaaaacgaa aaagcgcttc	1783

<210> 159  
 <211> 261  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 159

Met Lys Gln Arg Gln Asp Ala Trp Ser Glu Glu Asn Asp Leu Leu Leu
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20 25 30

Ala Phe Glu Glu Val Gly Asp Arg Leu Asn Arg Thr Ser Ala Ala Cys
35 40 45

Gly Phe Arg Trp Asn Ala Val Val Arg His Gln Tyr Glu Lys Ala Leu  
50 55 60

Gln Leu Ala Lys Lys Gln Arg Lys Gln Arg Met Arg Ala Leu Gly Asn  
65 70 75 80

Gly Gln Pro Ala Lys Lys Arg Leu Leu Tyr Lys Pro Pro Val Glu Thr  
85 90 95

Asn Ala Glu Pro Pro Ala Glu Ser Val Val Glu Gln Lys Lys Ala Thr  
100 105 110

Ala Asp Ser Ser Glu Gln Gln Pro Ile Ala Ser Glu His Leu Pro Tyr  
115 120 125

Val Asp Glu Ser Phe Lys Glu Glu Leu Ala Ser Leu Ser His Leu Leu  
130 135 140

Ser Pro Asn Gln Pro Gln Ala Gly His Thr Ala Asp Thr Ser Lys Asp  
145 150 155 160

Met Thr Ile Asp Asp Val Ile Arg Phe Leu Gln Asn Tyr Thr Gly Asn  
165 170 175

Glu Glu Gln Thr Ala Ala Leu Lys Met Glu Asn Glu Arg Leu Lys Gln  
180 185 190

Glu Asn Glu Glu Leu Thr Lys Lys Val Glu Lys Leu Glu Ala Glu Val  
195 200 205

Lys Lys Leu Glu Lys Asp Gln Thr Thr Ile Gln Glu Asp Tyr Glu Thr  
210 215 220

Leu Val Lys Ile Met Asn Arg Ala Arg Lys Leu Val Leu Phe Glu Glu  
225 230 235 240

Asp Glu His Ala Ala Pro Ala Phe Lys Met Asp Arg Asn Gly Asn Leu  
245 250 255

Glu Lys Met Ala Glu  
260

<210> 160  
 <211> 2311  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(1811)

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ctttgtattg gtgtttcagc gcttcagcgg acatatgctt cataagctga gcgaagaagg      180

ggtggtccgc gtgtgggaca gacactgcga gaaacatcgt tttgttgat ctgagctttc      240

gtgcagacgt gttcgggatg tagtccaatt tttcgatgac ttccaaaacc cgcttccttt      300

tttcttcaga tacatagggg tgatcggtca gtactcttga aacagttggt tttgacacat      360

tacttaattt tgcaatttcg tcaatcgtag gcataaagtc acttcctgaa aaaaagagtt      420

gttatggtat cgattccatc atttaagata tgtcatgaaa tatgacaatt tcccaaaaata      480

ataaaaaatgg ggtgaaattg atg aaa acc gca aac gaa aac atg act tgc acg      533
      Met Lys Thr Ala Asn Glu Asn Met Thr Cys Thr
      1             5             10

agc aaa cag cta ttt gtc ctt ctg aat gat ttg aag gaa gga aag ctc      581
Ser Lys Gln Leu Phe Val Leu Leu Asn Asp Leu Lys Glu Gly Lys Leu
      15             20             25

gct ggt gaa tgc cgt ata gac gac aca ctg gcc aat caa aaa tta aaa      629
Ala Gly Glu Cys Arg Ile Asp Asp Thr Leu Ala Asn Gln Lys Leu Lys
      30             35             40

gag aca ttg cag cag gat caa ttc gac ata acc gcc aat ttg ctg aac      677
Glu Thr Leu Gln Gln Asp Gln Phe Asp Ile Thr Ala Asn Leu Leu Asn
      45             50             55

aga atg gat tcc ccg ccc tcc aga gtt gac ttt atg ccg ctt cat cga      725
Arg Met Asp Ser Pro Pro Ser Arg Val Asp Phe Met Pro Leu His Arg
      60             65             70             75

ctg atc aca gaa gaa gaa gta gat gac gtg gtt cat gcg gtg aaa gac      773
Leu Ile Thr Glu Glu Glu Val Asp Asp Val Val His Ala Val Lys Asp
      80             85             90

gtg ctg ccg acc ggg caa ttt aca agc ggt ttt tat gtt ggc gta ttt      821
Val Leu Pro Thr Gly Gln Phe Thr Ser Gly Phe Tyr Val Gly Val Phe
      95             100            105

gaa gct gaa ata gct gct ttt ttg agc aaa aag cat gtc atg gct tca      869

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Glu	Ala	Glu	Ile	Ala	Ala	Phe	Leu	Ser	Lys	Lys	His	Val	Met	Ala	Ser		
		110					115					120					
tcc	agc	gga	acc	gat	gcc	atg	att	gtc	gcg	ctg	aag	gct	gcg	ggt	gtt		917
Ser	Ser	Gly	Thr	Asp	Ala	Met	Ile	Val	Ala	Leu	Lys	Ala	Ala	Gly	Val		
		125				130					135						
gga	caa	ggt	gat	gaa	gtc	att	atg	cct	gca	aac	agc	ttt	gct	gca	acg		965
Gly	Gln	Gly	Asp	Glu	Val	Ile	Met	Pro	Ala	Asn	Ser	Phe	Ala	Ala	Thr		
		140			145				150						155		
gaa	aac	gcc	gtg	ctc	gca	gct	gga	ggc	act	ccg	att	ttc	tgc	gat	att		1013
Glu	Asn	Ala	Val	Leu	Ala	Ala	Gly	Gly	Thr	Pro	Ile	Phe	Cys	Asp	Ile		
			160					165						170			
gac	cct	gtt	aca	ttt	tgc	atg	gat	cct	tca	gaa	att	gaa	gca	tgt	gtc		1061
Asp	Pro	Val	Thr	Phe	Cys	Met	Asp	Pro	Ser	Glu	Ile	Glu	Ala	Cys	Val		
			175					180						185			
act	ttg	aaa	acg	aaa	tgc	att	ttg	cct	gta	cac	ctt	tat	gga	aag	ctg		1109
Thr	Leu	Lys	Thr	Lys	Cys	Ile	Leu	Pro	Val	His	Leu	Tyr	Gly	Lys	Leu		
		190					195					200					
cct	gac	atg	gaa	gcc	att	gca	aaa	acc	gct	gat	aaa	tac	ggc	atc	ccg		1157
Pro	Asp	Met	Glu	Ala	Ile	Ala	Lys	Thr	Ala	Asp	Lys	Tyr	Gly	Ile	Pro		
		205				210					215						
att	att	gaa	gac	gcc	tgc	cag	gcg	atc	ggc	gtt	tcc	gat	ctg	gga	aaa		1205
Ile	Ile	Glu	Asp	Ala	Cys	Gln	Ala	Ile	Gly	Val	Ser	Asp	Leu	Gly	Lys		
		220			225				230						235		
aac	agc	ctt	tgc	tcc	ata	tta	agc	ttc	aat	ccg	tat	aaa	aat	ctc	ggc		1253
Asn	Ser	Leu	Cys	Ser	Ile	Leu	Ser	Phe	Asn	Pro	Tyr	Lys	Asn	Leu	Gly		
			240					245						250			
act	tgc	gga	aaa	gcc	ggc	gca	att	gtg	acg	gat	gat	cca	tca	ttt	gca		1301
Thr	Cys	Gly	Lys	Ala	Gly	Ala	Ile	Val	Thr	Asp	Asp	Pro	Ser	Phe	Ala		
			255					260						265			
tcc	gca	tgc	atg	gaa	tat	atg	tat	cac	ggc	ttt	gaa	ctg	aat	caa	aaa		1349
Ser	Ala	Cys	Met	Glu	Tyr	Met	Tyr	His	Gly	Phe	Glu	Leu	Asn	Gln	Lys		
		270				275						280					
aat	aaa	aag	gcg	gct	gac	tac	ggc	ttt	aac	gct	aag	att	gat	aat	ctg		1397
Asn	Lys	Lys	Ala	Ala	Asp	Tyr	Gly	Phe	Asn	Ala	Lys	Ile	Asp	Asn	Leu		
		285				290					295						
caa	gcc	gct	att	gga	ctg	gca	agg	atg	aaa	tat	ctt	tct	tta	aat	aat		1445
Gln	Ala	Ala	Ile	Gly	Leu	Ala	Arg	Met	Lys	Tyr	Leu	Ser	Leu	Asn	Asn		
					305				310						315		
ctg	aag	cgc	tta	tat	tta	gca	gat	cgt	tat	att	gcg	cat	ttg	cag	cag		1493
Leu	Lys	Arg	Leu	Tyr	Leu	Ala	Asp	Arg	Tyr	Ile	Ala	His	Leu	Gln	Gln		
			320					325						330			
tat	gaa	gac	aga	ggt	ctg	atc	aaa	ttg	cct	caa	atg	acc	gat	gat	cat		1541
Tyr	Glu	Asp	Arg	Gly	Leu	Ile	Lys	Leu	Pro	Gln	Met	Thr	Asp	Asp	His		

335	340	345	
gta tgg cat ttg ttt aca att aaa ata cta aac gga aat cgt gac caa			1589
Val Trp His Leu Phe Thr Ile Lys Ile Leu Asn Gly Asn Arg Asp Gln			
350	355	360	
gtc aaa gat atg atg ctt aaa ttt cat aat gtc caa aca gat ata tac			1637
Val Lys Asp Met Met Leu Lys Phe His Asn Val Gln Thr Asp Ile Tyr			
365	370	375	
tac ccg att tta tcc cat cat caa aac aca cca ctt gta aaa gcc aat			1685
Tyr Pro Ile Leu Ser His His Gln Asn Thr Pro Leu Val Lys Ala Asn			
380	385	390	395
tat cgg cac aca tca ctg ccg gtc act gaa tca gtg cat aaa caa atg			1733
Tyr Arg His Thr Ser Leu Pro Val Thr Glu Ser Val His Lys Gln Met			
400	405	410	
ctt cag ctt cct ctc tat ccg ggg ctc acc gta gaa gaa caa gac aaa			1781
Leu Gln Leu Pro Leu Tyr Pro Gly Leu Thr Val Glu Glu Gln Asp Lys			
415	420	425	
gta atg gag gcc tta att gat gtc gta tca tgaaacactt tcttttcaca			1831
Val Met Glu Ala Leu Ile Asp Val Val Ser			
430	435		
ccttgcagca agtaaacaag ccgaagtacg ccgtatttttg cgatttttgat gagacatatt			1891
tcgcccacag catcaccgat gaatcgagaa aagcgctcat ggaccttgaa acatttattc			1951
attcgcacca tcttgatcac aagatttttg cgggctgggt gaccgggagc agcctgtcat			2011
ccgttcttgc aaaaatgaag cggggaggct ttcgatatct tccgcatttt gtcgccggtg			2071
accttggcac tgaaatcact tatttctctg aagaaggcca agtctctgat aaagattggg			2131
aagcccgatt gcaagaatca aatttctccc atgatctgggt cgaagaaatc aagcagactc			2191
tctctaataaaa atatgagatt gcgcttgtgc ctcagactca gcatggcttt tcccgtata			2251
aaatcaacta ttactataaa tcgttgaag agagcataga taagagggcg cttgaagcca			2311

<210> 161

<211> 437

<212> PRT

<213> Bacillus licheniformis

<400> 161

Met	Lys	Thr	Ala	Asn	Glu	Asn	Met	Thr	Cys	Thr	Ser	Lys	Gln	Leu	Phe
1				5				10						15	

Val	Leu	Leu	Asn	Asp	Leu	Lys	Glu	Gly	Lys	Leu	Ala	Gly	Glu	Cys	Arg
			20					25					30		

Ile Asp Asp Thr Leu Ala Asn Gln Lys Leu Lys Glu Thr Leu Gln Gln  
35 40 45

Asp Gln Phe Asp Ile Thr Ala Asn Leu Leu Asn Arg Met Asp Ser Pro  
50 55 60

Pro Ser Arg Val Asp Phe Met Pro Leu His Arg Leu Ile Thr Glu Glu  
65 70 75 80

Glu Val Asp Asp Val Val His Ala Val Lys Asp Val Leu Pro Thr Gly  
85 90 95

Gln Phe Thr Ser Gly Phe Tyr Val Gly Val Phe Glu Ala Glu Ile Ala  
100 105 110

Ala Phe Leu Ser Lys Lys His Val Met Ala Ser Ser Ser Gly Thr Asp  
115 120 125

Ala Met Ile Val Ala Leu Lys Ala Ala Gly Val Gly Gln Gly Asp Glu  
130 135 140

Val Ile Met Pro Ala Asn Ser Phe Ala Ala Thr Glu Asn Ala Val Leu  
145 150 155 160

Ala Ala Gly Gly Thr Pro Ile Phe Cys Asp Ile Asp Pro Val Thr Phe  
165 170 175

Cys Met Asp Pro Ser Glu Ile Glu Ala Cys Val Thr Leu Lys Thr Lys  
180 185 190

Cys Ile Leu Pro Val His Leu Tyr Gly Lys Leu Pro Asp Met Glu Ala  
195 200 205

Ile Ala Lys Thr Ala Asp Lys Tyr Gly Ile Pro Ile Ile Glu Asp Ala  
210 215 220

Cys Gln Ala Ile Gly Val Ser Asp Leu Gly Lys Asn Ser Leu Cys Ser  
225 230 235 240

Ile Leu Ser Phe Asn Pro Tyr Lys Asn Leu Gly Thr Cys Gly Lys Ala  
245 250 255

Gly Ala Ile Val Thr Asp Asp Pro Ser Phe Ala Ser Ala Cys Met Glu  
260 265 270

Tyr Met Tyr His Gly Phe Glu Leu Asn Gln Lys Asn Lys Lys Ala Ala  
275 280 285

Asp Tyr Gly Phe Asn Ala Lys Ile Asp Asn Leu Gln Ala Ala Ile Gly  
290 295 300

Leu Ala Arg Met Lys Tyr Leu Ser Leu Asn Asn Leu Lys Arg Leu Tyr  
305 310 315 320

Leu Ala Asp Arg Tyr Ile Ala His Leu Gln Gln Tyr Glu Asp Arg Gly  
325 330 335

Leu Ile Lys Leu Pro Gln Met Thr Asp Asp His Val Trp His Leu Phe  
340 345 350

Thr Ile Lys Ile Leu Asn Gly Asn Arg Asp Gln Val Lys Asp Met Met  
355 360 365

Leu Lys Phe His Asn Val Gln Thr Asp Ile Tyr Tyr Pro Ile Leu Ser  
370 375 380

His His Gln Asn Thr Pro Leu Val Lys Ala Asn Tyr Arg His Thr Ser  
385 390 395 400

Leu Pro Val Thr Glu Ser Val His Lys Gln Met Leu Gln Leu Pro Leu  
405 410 415

Tyr Pro Gly Leu Thr Val Glu Glu Gln Asp Lys Val Met Glu Ala Leu  
420 425 430

Ile Asp Val Val Ser  
435

<210> 162  
<211> 2143  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(1643)



<400> 162

gctgccgcag aagaacttgc gcggcttcat ccggacgcga agttcgtcct ggctgtcggc 60

caaaacagca tcagacagca gctgtatgaa cgcattggtc ttccgcttga ccggtatgcg 120

gttttgattc atccctctgc tggtgtcagc ggttcggccc ggattcaaaa cggcgccgtt 180

gttatggcat cgagcgtcat ccaagcggat gcagacgtcg gcatccacgc gattgtcaac 240

acaggtgcga tcgtcgaaca cgacaatcgg atcggcgatt acgttcatct ttcgcccgga 300

acggtgttaa ccggcggcgt gacagttatg gaaggcgctc atctcggcgc gggaacggcg 360

gtcattcccg gaaagacagt cggacgtcgg agcgtgacgg gagcgggggc agccgtgatt 420

cacgacattc ctgataattg caccgcagtc ggagtccttg caagaatgat caaataacag 480

cagtaaaaag ggtgaaaaac atg agt cag aat aag cga att tat tta tca ccg 533

Met Ser Gln Asn Lys Arg Ile Tyr Leu Ser Pro

1 5 10

ccg cac atg agc gga gac gag gag cgc tat gta gcc gaa gcg ttt cgg 581

Pro His Met Ser Gly Asp Glu Glu Arg Tyr Val Ala Glu Ala Phe Arg

15 20 25

aca aac tgg atc gcg ccc ctg ggt ccc ctt gtc gac aca ttt gaa gaa 629

Thr Asn Trp Ile Ala Pro Leu Gly Pro Leu Val Asp Thr Phe Glu Glu

30 35 40

aag ctt gcc gcc tat gcg ggg acg tcc gga gcc gcg gca gtc agc tca 677

Lys Leu Ala Ala Tyr Ala Gly Thr Ser Gly Ala Ala Ala Val Ser Ser

45 50 55

gga aca gct gcg atc cac ctg gcc ttg aaa ttg ctg ggc gtc ggc aaa 725

Gly Thr Ala Ala Ile His Leu Ala Leu Lys Leu Leu Gly Val Gly Lys

60 65 70 75

ggc gat acg gtc ttc tgc tct tct ttt acg ttt gta gcg agc gcc aat 773

Gly Asp Thr Val Phe Cys Ser Ser Phe Thr Phe Val Ala Ser Ala Asn

80 85 90

ccg atc ata tat gag cag gct gaa ccg gtt ttc att gat tct gaa cgg 821

Pro Ile Ile Tyr Glu Gln Ala Glu Pro Val Phe Ile Asp Ser Glu Arg

95 100 105

gat aca tgg aac atg tcg ccc gag gcg ctt gaa cgg gcg ctt gac gaa 869

Asp Thr Trp Asn Met Ser Pro Glu Ala Leu Glu Arg Ala Leu Asp Glu

110 115 120

gcg gag cgg gcc agg aat ctg ccg aaa gcc gtc atc gtc gtc aac ttg 917

Ala Glu Arg Ala Arg Asn Leu Pro Lys Ala Val Ile Val Val Asn Leu

125 130 135

tac ggc caa agc gcg aaa atg gac gag att atg gcc att tgc gat cga 965

Tyr Gly Gln Ser Ala Lys Met Asp Glu Ile Met Ala Ile Cys Asp Arg

140 145 150 155

ttt gcc gtg cct gtc att gaa gat gca gcc gaa tcg ctc ggt tct gtt	1013
Phe Ala Val Pro Val Ile Glu Asp Ala Ala Glu Ser Leu Gly Ser Val	
160 165 170	
tat aaa ggc aga aaa agc ggg acc ttc gga cgc ttc ggc att tat tcg	1061
Tyr Lys Gly Arg Lys Ser Gly Thr Phe Gly Arg Phe Gly Ile Tyr Ser	
175 180 185	
ttc aac ggt aac aaa atc atc acc aca tcg ggc gga gga atg ctg gtc	1109
Phe Asn Gly Asn Lys Ile Ile Thr Thr Ser Gly Gly Gly Met Leu Val	
190 195 200	
agc gat gat <sup>^</sup> gaa gac gcg ttg aag aag gcg cgc ttt tta gcc act cag	1157
Ser Asp Asp Glu Asp Ala Leu Lys Lys Ala Arg Phe Leu Ala Thr Gln	
205 210 215	
gcg cgc gag cca gcc att cat tat cag cac gaa aaa gcg ggc tac aat	1205
Ala Arg Glu Pro Ala Ile His Tyr Gln His Glu Lys Ala Gly Tyr Asn	
220 225 230 235	
tac cgg atg agc aat gtt ctg gcc gga atc ggc atc gca cag ctc gcc	1253
Tyr Arg Met Ser Asn Val Leu Ala Gly Ile Gly Ile Ala Gln Leu Ala	
240 245 250	
gtt ctg gat gac cgg gta cat gcc aga cgg gcg gtt ttc gag cgc tat	1301
Val Leu Asp Asp Arg Val His Ala Arg Arg Ala Val Phe Glu Arg Tyr	
255 260 265	
aag gag gcg ctt tcc ggt atc gaa ggt ata gaa ttc atg cct gag gcc	1349
Lys Glu Ala Leu Ser Gly Ile Glu Gly Ile Glu Phe Met Pro Glu Ala	
270 275 280	
ggc atg tca aac cgc tgg ctc acg aca tta acg tta gac aca gca aag	1397
Gly Met Ser Asn Arg Trp Leu Thr Thr Leu Thr Leu Asp Thr Ala Lys	
285 290 295	
att caa aca aca ccg gcg gac atc atc gaa cag ctc gca aat gaa aac	1445
Ile Gln Thr Thr Pro Ala Asp Ile Ile Glu Gln Leu Ala Asn Glu Asn	
300 305 310 315	
att gag gcc cgc ccg tta tgg aag cct ttg cac aga cag ccc ctt ttt	1493
Ile Glu Ala Arg Pro Leu Trp Lys Pro Leu His Arg Gln Pro Leu Phe	
320 325 330	
aaa ggc gcg gcc ttt tat ccg cac gat gac cag ggc tct gtc tgc tgc	1541
Lys Gly Ala Ala Phe Tyr Pro His Asp Asp Gln Gly Ser Val Cys Cys	
335 340 345	
gac tta ttt cag cgc ggg ctc tgc ctg ccg tca gga tca agt atg acg	1589
Asp Leu Phe Gln Arg Gly Leu Cys Leu Pro Ser Gly Ser Ser Met Thr	
350 355 360	
cga aaa gag cag gac ccg gta att caa atc gtt gcc gac ccg att aaa	1637
Arg Lys Glu Gln Asp Arg Val Ile Gln Ile Val Ala Asp Arg Ile Lys	
365 370 375	

tat aaa tgagggtgcta aacatggcga ttacatatcc catggacagc ttaaagcata 1693  
Tyr Lys  
380

agctggcaga aattttggat gtcattccaa ggcattcatc agtcgtttac ttggactacc 1753  
cgctatacgg aaacgtcggg gatctattga tcatgaaagg aacggaagct ttttttgaag 1813  
catacggcat caagggtcgc gaaagatgga atgcggagaa tttcattccg ggccgccgca 1873  
ttccaaagga cgccatcatt gtttgtcagg ggggcggcaa tttcggcgac ttgtaccctc 1933  
acttccagca gttcagagaa cgggtggtcg aacattaccc ggacaaccgg atcgtcattc 1993  
tgccgcagtc gatttattat gagcatgaag aaaatataat aaaaacgcgc ggcattttgg 2053  
cggctcaccg ggatctgcac ttattcacgc gggaaaaggc atcattcgat tttgccgtca 2113  
agcgtttcga agagggtgaaa aacatcaaaa 2143

<210> 163  
<211> 381  
<212> PRT  
<213> Bacillus licheniformis

<400> 163

Met Ser Gln Asn Lys Arg Ile Tyr Leu Ser Pro Pro His Met Ser Gly  
1 5 10 15

Asp Glu Glu Arg Tyr Val Ala Glu Ala Phe Arg Thr Asn Trp Ile Ala  
20 25 30

Pro Leu Gly Pro Leu Val Asp Thr Phe Glu Glu Lys Leu Ala Ala Tyr  
35 40 45

Ala Gly Thr Ser Gly Ala Ala Ala Val Ser Ser Gly Thr Ala Ala Ile  
50 55 60

His Leu Ala Leu Lys Leu Leu Gly Val Gly Lys Gly Asp Thr Val Phe  
65 70 75 80

Cys Ser Ser Phe Thr Phe Val Ala Ser Ala Asn Pro Ile Ile Tyr Glu  
85 90 95

Gln Ala Glu Pro Val Phe Ile Asp Ser Glu Arg Asp Thr Trp Asn Met  
100 105 110

Ser Pro Glu Ala Leu Glu Arg Ala Leu Asp Glu Ala Glu Arg Ala Arg

115	120	125
Asn Leu Pro Lys Ala Val Ile Val Val Asn Leu Tyr Gly Gln Ser Ala 130 135 140		
Lys Met Asp Glu Ile Met Ala Ile Cys Asp Arg Phe Ala Val Pro Val 145 150 155 160		
Ile Glu Asp Ala Ala Glu Ser Leu Gly Ser Val Tyr Lys Gly Arg Lys 165 170 175		
Ser Gly Thr Phe Gly Arg Phe Gly Ile Tyr Ser Phe Asn Gly Asn Lys 180 185 190		
Ile Ile Thr Thr Ser Gly Gly Gly Met Leu Val Ser Asp Asp Glu Asp 195 200 205		
Ala Leu Lys Lys Ala Arg Phe Leu Ala Thr Gln Ala Arg Glu Pro Ala 210 215 220		
Ile His Tyr Gln His Glu Lys Ala Gly Tyr Asn Tyr Arg Met Ser Asn 225 230 235 240		
Val Leu Ala Gly Ile Gly Ile Ala Gln Leu Ala Val Leu Asp Asp Arg 245 250 255		
Val His Ala Arg Arg Ala Val Phe Glu Arg Tyr Lys Glu Ala Leu Ser 260 265 270		
Gly Ile Glu Gly Ile Glu Phe Met Pro Glu Ala Gly Met Ser Asn Arg 275 280 285		
Trp Leu Thr Thr Leu Thr Leu Asp Thr Ala Lys Ile Gln Thr Thr Pro 290 295 300		
Ala Asp Ile Ile Glu Gln Leu Ala Asn Glu Asn Ile Glu Ala Arg Pro 305 310 315 320		
Leu Trp Lys Pro Leu His Arg Gln Pro Leu Phe Lys Gly Ala Ala Phe 325 330 335		
Tyr Pro His Asp Asp Gln Gly Ser Val Cys Cys Asp Leu Phe Gln Arg 340 345 350		

Gly Leu Cys Leu Pro Ser Gly Ser Ser Met Thr Arg Lys Glu Gln Asp  
 355 360 365

Arg Val Ile Gln Ile Val Ala Asp Arg Ile Lys Tyr Lys  
 370 375 380

<210> 164  
 <211> 2107  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1607)

<400> 164  
 gactgccacc gctttctcgg cgacatggac aatgagctga gatctctgtt ccagtcattt 60  
 gaatttttcta aaacgcctcg tgccgaaaca tgctcaagaa tcggctataa ctttcagcgg 120  
 aggcgggaat acaaggccgc tatctactgg tatgagctgg ccacaacatt ggtgcctgat 180  
 tcaaataaat ggagcttcac ctatccggca tactatactt ggtaccctca tttgcaaata 240  
 tgtgtgtgct attacaattt aggagacttt gaaaagtcgt atcatcataa tgaagaggcg 300  
 aggaaatacc gtcccgaaga caaatccgtc cttcataaca aacagctgct ggaagggaaa 360  
 ttaggcatta acaattagca ttgtaaagac ttactgaaca agtaggtctt ttttttatga 420  
 ataaaaatcaa gccgtgccaa tttagcggca ggcatcataa cttatttttg aactttttga 480  
 atttagagga ggaacaaagg atg atc ccg tta gtc aat tta aaa cgt caa ttt 533  
 Met Ile Pro Leu Val Asn Leu Lys Arg Gln Phe  
 1 5 10  
 caa aca gta aaa cag gat att tta aaa gag ttt gaa cat gtg ctg gac 581  
 Gln Thr Val Lys Gln Asp Ile Leu Lys Glu Phe Glu His Val Leu Asp  
 15 20 25  
 agc ggc caa tat ata ttg ggg cca aag gtt gaa gaa tta gag aaa aga 629  
 Ser Gly Gln Tyr Ile Leu Gly Pro Lys Val Glu Glu Leu Glu Lys Arg  
 30 35 40  
 ata gct gaa aag ctt ggt gta aaa gaa gcg gtc gcg gtc gcc aac gga 677  
 Ile Ala Glu Lys Leu Gly Val Lys Glu Ala Val Ala Val Ala Asn Gly  
 45 50 55  
 acg gat gca ttg gtg ctg acg ctt gaa gct ttc ggc atc ggc aaa ggg 725  
 Thr Asp Ala Leu Val Leu Thr Leu Glu Ala Phe Gly Ile Gly Lys Gly  
 60 65 70 75

gat gaa gtg att acg acc ccg ttc act ttt ttc gcc acc gcc gaa gcc	773
Asp Glu Val Ile Thr Thr Pro Phe Thr Phe Phe Ala Thr Ala Glu Ala	
80 85 90	
gtc tca agg gtg ggg gct gaa cct gtg ttt gct gat gtc gat cct gaa	821
Val Ser Arg Val Gly Ala Glu Pro Val Phe Ala Asp Val Asp Pro Glu	
95 100 105	
aca tac aat ctt gat ccg aaa aaa ata gaa gaa aag atc acc cct gct	869
Thr Tyr Asn Leu Asp Pro Lys Lys Ile Glu Glu Lys Ile Thr Pro Ala	
110 115 120	
act aaa gcg atc att ccc gtc cat atc ttc gga cag ccg gct gat atg	917
Thr Lys Ala Ile Ile Pro Val His Ile Phe Gly Gln Pro Ala Asp Met	
125 130 135	
gac gag atc atg gag ctt gcc aaa aaa cac gga ctg ctt gtg att gag	965
Asp Glu Ile Met Glu Leu Ala Lys Lys His Gly Leu Leu Val Ile Glu	
140 145 150 155	
gat gcc tgc caa gcg ttc ggc gca tcg tat aaa gag cgg cct gtc ggc	1013
Asp Ala Cys Gln Ala Phe Gly Ala Ser Tyr Lys Glu Arg Pro Val Gly	
160 165 170	
agc atc ggg gat gcc gcc tgt ttt tca ttt ttc cct aca aaa aac ttg	1061
Ser Ile Gly Asp Ala Ala Cys Phe Ser Phe Phe Pro Thr Lys Asn Leu	
175 180 185	
gga aca ttg gga gac ggg gga atg gtg acg att tca gac ccg gat gca	1109
Gly Thr Leu Gly Asp Gly Gly Met Val Thr Ile Ser Asp Pro Asp Ala	
190 195 200	
gcc cgg caa tta aga aca ctc aga acc cat ggc act agc aaa aaa tac	1157
Ala Arg Gln Leu Arg Thr Leu Arg Thr His Gly Thr Ser Lys Lys Tyr	
205 210 215	
ttc cat gac aaa atc ggt ttc aac agc cgt ctt gat gaa tta cac gcc	1205
Phe His Asp Lys Ile Gly Phe Asn Ser Arg Leu Asp Glu Leu His Ala	
220 225 230 235	
gca gct tta ctc att ctt ctt gag aaa atc gac ggc tgg aat gaa caa	1253
Ala Ala Leu Leu Ile Leu Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln	
240 245 250	
aga aga aga gtg gcc agc cgc tac aga gaa ggt ttg aaa acg gcg gag	1301
Arg Arg Arg Val Ala Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu	
255 260 265	
cac ctc aca ctg ccg gca gag aaa gag gac cgc aca cat atc tat cat	1349
His Leu Thr Leu Pro Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His	
270 275 280	
ctc tat tgt atc ggc gcg aaa aac cgc gac tac atc ata caa tcg ctg	1397
Leu Tyr Cys Ile Gly Ala Lys Asn Arg Asp Tyr Ile Ile Gln Ser Leu	
285 290 295	
aaa gag cag gac att cat tca ggt gtg tat tat cct tgc tgc ctt cat	1445

Lys Glu Gln Asp Ile His Ser Gly Val Tyr Tyr Pro Cys Cys Leu His  
 300 305 310 315  
 ctg caa tcg gtc tat tct tca ctg cag tac aaa aaa ggc gat ttt cct 1493  
 Leu Gln Ser Val Tyr Ser Ser Leu Gln Tyr Lys Lys Gly Asp Phe Pro  
 320 325 330  
 ata gcc gag tcc ttg tcc gaa acc ctt ttc gcc att ccg atg gat cct 1541  
 Ile Ala Glu Ser Leu Ser Glu Thr Leu Phe Ala Ile Pro Met Asp Pro  
 335 340 345  
 ttt cta gcc gcc gag gaa caa gat cag att att tct gcg ctg ctg aaa 1589  
 Phe Leu Ala Ala Glu Glu Gln Asp Gln Ile Ile Ser Ala Leu Leu Lys  
 350 355 360  
 aaa gga gga ggg gaa aag tgacgggttca ttttggttta atcggctgcg 1637  
 Lys Gly Gly Gly Glu Lys  
 365  
 gctatatgtc aagaaaacat cttcaagcac tggccgagtg cgatgatgca aagttgtcgg 1697  
 ccgtcagtga tttgcaggaa gaaagaatga aggaagcggg agaatactat gcttcctcgg 1757  
 ccggtgagga aagccgaatg acccgctatc cgcagtatca agcgctgctt tcagatccta 1817  
 aaattgaagc ggtcattatt gcggcgggtt cgggactgca cgccgaaatg gccaaacatg 1877  
 cgctgctggc aggcaagcac gtcacgctcg aaaaaccgat gaccttgtca ttacgggatg 1937  
 ccgatgagct tatagaactg gcggagcaga acgggctgaa gctcatggtc tgccaccaga 1997  
 tgcgccaccg gccgatcatg aaaaaactga aggaaacgat tgaggaagga aagctgggaa 2057  
 agatctactt gggcacggta tcgctccgct taaacaggtc ccccgcttat 2107

<210> 165

<211> 369

<212> PRT

<213> Bacillus licheniformis

<400> 165

Met Ile Pro Leu Val Asn Leu Lys Arg Gln Phe Gln Thr Val Lys Gln  
 1 5 10 15

Asp Ile Leu Lys Glu Phe Glu His Val Leu Asp Ser Gly Gln Tyr Ile  
 20 25 30

Leu Gly Pro Lys Val Glu Glu Leu Glu Lys Arg Ile Ala Glu Lys Leu  
 35 40 45

Gly Val Lys Glu Ala Val Ala Val Ala Asn Gly Thr Asp Ala Leu Val  
 50 55 60

Leu Thr Leu Glu Ala Phe Gly Ile Gly Lys Gly Asp Glu Val Ile Thr  
65 70 75 80

Thr Pro Phe Thr Phe Phe Ala Thr Ala Glu Ala Val Ser Arg Val Gly  
85 90 95

Ala Glu Pro Val Phe Ala Asp Val Asp Pro Glu Thr Tyr Asn Leu Asp  
100 105 110

Pro Lys Lys Ile Glu Glu Lys Ile Thr Pro Ala Thr Lys Ala Ile Ile  
115 120 125

Pro Val His Ile Phe Gly Gln Pro Ala Asp Met Asp Glu Ile Met Glu  
130 135 140

Leu Ala Lys Lys His Gly Leu Leu Val Ile Glu Asp Ala Cys Gln Ala  
145 150 155 160

Phe Gly Ala Ser Tyr Lys Glu Arg Pro Val Gly Ser Ile Gly Asp Ala  
165 170 175

Ala Cys Phe Ser Phe Phe Pro Thr Lys Asn Leu Gly Thr Leu Gly Asp  
180 185 190

Gly Gly Met Val Thr Ile Ser Asp Pro Asp Ala Ala Arg Gln Leu Arg  
195 200 205

Thr Leu Arg Thr His Gly Thr Ser Lys Lys Tyr Phe His Asp Lys Ile  
210 215 220

Gly Phe Asn Ser Arg Leu Asp Glu Leu His Ala Ala Ala Leu Leu Ile  
225 230 235 240

Leu Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln Arg Arg Arg Val Ala  
245 250 255

Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu His Leu Thr Leu Pro  
260 265 270

Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His Leu Tyr Cys Ile Gly  
275 280 285



Ala Lys Asn Arg Asp Tyr Ile Ile Gln Ser Leu Lys Glu Gln Asp Ile  
 290 295 300

His Ser Gly Val Tyr Tyr Pro Cys Cys Leu His Leu Gln Ser Val Tyr  
 305 310 315 320

Ser Ser Leu Gln Tyr Lys Lys Gly Asp Phe Pro Ile Ala Glu Ser Leu  
 325 330 335

Ser Glu Thr Leu Phe Ala Ile Pro Met Asp Pro Phe Leu Ala Ala Glu  
 340 345 350

Glu Gln Asp Gln Ile Ile Ser Ala Leu Leu Lys Lys Gly Gly Gly Glu  
 355 360 365

Lys

<210> 166  
 <211> 2092  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1592)

<400> 166  
 ctttcccagc ttgggggctg tggcgaaaat gtcgttatcg aagacggggt ccgcattttt 60  
 catccggaac acatctatat cggagataac gtttatatcg gccatgacac gatttttaaaa 120  
 ggctattata agcatgacct gatcatcggg tcaaacagct ggatcgggca gcaatgtttt 180  
 atacacgggtg ccggcggggt tacaatcgga gaatttgcag gaattgggtcc gaacgtccgg 240  
 atacatgccg cttaccatac cgatcctgat aaacccgaca gtaccatttt gttttcgccg 300  
 cttacattcg ctctattca tattgaagaa aactgcaaca tcgggatcgg tgcgtctatc 360  
 ctagcaggcg ttacgatagg cgccactcc aaaatcggag caaatgccgt cgtcaatcgc 420  
 aatattcccc cgtacagcat agcagtaggc gtgccggcaa aggtgattaa aaaccgaaga 480  
 atgaaagatg aggatctctc atg atc aga ttg atc gag ccg tat att aca ttt 533  
 Met Ile Arg Leu Ile Glu Pro Tyr Ile Thr Phe  
 1 5 10  
 gaa gaa gtg caa gca gaa tta aag gag ata ttt tcc tct ggc atg ctg 581

Glu	Glu	Val	Gln	Ala	Glu	Leu	Lys	Glu	Ile	Phe	Ser	Ser	Gly	Met	Leu		
			15					20					25				
aca	aaa	ggc	cct	tat	gtc	aga	aca	ttt	gct	gat	cat	atg	aga	cag	tat	629	
Thr	Lys	Gly	Pro	Tyr	Val	Arg	Thr	Phe	Ala	Asp	His	Met	Arg	Gln	Tyr		
		30					35					40					
gtc	agt	gca	aag	cat	gct	ttt	tta	aca	aca	tcg	gca	aca	acg	gct	tta	677	
Val	Ser	Ala	Lys	His	Ala	Phe	Leu	Thr	Thr	Ser	Ala	Thr	Thr	Ala	Leu		
		45				50					55						
tcg	atg	tgc	ctt	aaa	agc	ctg	aac	gtg	caa	ccc	gga	gat	gaa	gta	atc	725	
Ser	Met	Cys	Leu	Lys	Ser	Leu	Asn	Val	Gln	Pro	Gly	Asp	Glu	Val	Ile		
60					65				70						75		
gtc	tca	gac	ttc	tcg	ttc	ccc	gcc	act	gtc	aat	gta	ata	gaa	gat	tta	773	
Val	Ser	Asp	Phe	Ser	Phe	Pro	Ala	Thr	Val	Asn	Val	Ile	Glu	Asp	Leu		
			80						85					90			
gga	gcc	aag	ccg	gtt	ttt	gcc	gat	gtt	gat	ctt	gaa	aca	ttt	aac	atg	821	
Gly	Ala	Lys	Pro	Val	Phe	Ala	Asp	Val	Asp	Leu	Glu	Thr	Phe	Asn	Met		
			95					100					105				
ctt	cca	gaa	gaa	ctg	gaa	agt	caa	atc	acg	tcc	cgt	aca	aaa	gcc	gtt	869	
Leu	Pro	Glu	Glu	Leu	Glu	Ser	Gln	Ile	Thr	Ser	Arg	Thr	Lys	Ala	Val		
		110					115					120					
ctt	ttt	gta	gat	gct	ctt	gga	aac	ccg	aca	ggc	atc	acc	aac	att	aag	917	
Leu	Phe	Val	Asp	Ala	Leu	Gly	Asn	Pro	Thr	Gly	Ile	Thr	Asn	Ile	Lys		
		125				130					135						
caa	att	tgt	aag	gag	tac	ggc	tta	ccc	ctt	gtg	gat	gat	gcc	gct	tgt	965	
Gln	Ile	Cys	Lys	Glu	Tyr	Gly	Leu	Pro	Leu	Val	Asp	Asp	Ala	Ala	Cys		
140					145					150					155		
gcg	atc	ggc	agc	agc	gaa	tac	ggc	tgt	aaa	tcc	gga	aaa	att	gcc	gat	1013	
Ala	Ile	Gly	Ser	Ser	Glu	Tyr	Gly	Cys	Lys	Ser	Gly	Lys	Ile	Ala	Asp		
				160					165					170			
ctc	acc	tgt	ttc	agc	ttt	cac	cca	aga	aag	ctg	ctt	acg	aca	ggc	gaa	1061	
Leu	Thr	Cys	Phe	Ser	Phe	His	Pro	Arg	Lys	Leu	Leu	Thr	Thr	Gly	Glu		
			175					180					185				
ggc	ggg	gca	att	aca	acc	gac	cgg	gaa	gag	ttg	aaa	gac	tgg	ctt	tcg	1109	
Gly	Gly	Ala	Ile	Thr	Thr	Asp	Arg	Glu	Glu	Leu	Lys	Asp	Trp	Leu	Ser		
		190					195					200					
gtc	aaa	tta	aac	cat	ggc	gct	gcc	atc	tct	gac	gga	aaa	ttg	gat	ttt	1157	
Val	Lys	Leu	Asn	His	Gly	Ala	Ala	Ile	Ser	Asp	Gly	Lys	Leu	Asp	Phe		
		205				210					215						
ata	gat	ttc	ggc	tac	aac	tac	aga	tta	tcc	gat	atc	caa	gcc	gct	ctt	1205	
Ile	Asp	Phe	Gly	Tyr	Asn	Tyr	Arg	Leu	Ser	Asp	Ile	Gln	Ala	Ala	Leu		
220					225					230					235		
gga	att	aaa	cag	ctc	caa	aaa	ctt	gat	gac	atc	att	cat	cgg	aga	aac	1253	
Gly	Ile	Lys	Gln	Leu	Gln	Lys	Leu	Asp	Asp	Ile	Ile	His	Arg	Arg	Asn		

240	245	250	
ctt cag cag aaa gca tat agt gaa cag ctt gaa ccc ctc gga ttc caa			1301
Leu Gln Gln Lys Ala Tyr Ser Glu Gln Leu Glu Pro Leu Gly Phe Gln			
255	260	265	
agt caa aaa atc ggt cca gcc gtt gta cac aac ata caa tcc gcc gtt			1349
Ser Gln Lys Ile Gly Pro Ala Val Val His Asn Ile Gln Ser Ala Val			
270	275	280	
ttc aaa gtt cca aaa aac atc gtt cgc gac gaa ttg att caa tat ttg			1397
Phe Lys Val Pro Lys Asn Ile Val Arg Asp Glu Leu Ile Gln Tyr Leu			
285	290	295	
agc gac tgc cat ata gag tcg act ttc ggc act tat tgt tta agc ggc			1445
Ser Asp Cys His Ile Glu Ser Thr Phe Gly Thr Tyr Cys Leu Ser Gly			
300	305	310	315
act ccc tat tac cgc cgg aaa tac caa cag cta aaa tcg aat tct ctc			1493
Thr Pro Tyr Tyr Arg Arg Lys Tyr Gln Gln Leu Lys Ser Asn Ser Leu			
320	325	330	
ttt ctt gaa caa cat acg att acc ctc cct tgc cat gat gaa gtc gat			1541
Phe Leu Glu Gln His Thr Ile Thr Leu Pro Cys His Asp Glu Val Asp			
335	340	345	
tta gat cat gtg gtt tca gcc ata caa tca ttt atc aaa ttt aag gtt			1589
Leu Asp His Val Val Ser Ala Ile Gln Ser Phe Ile Lys Phe Lys Val			
350	355	360	
gat tagttcaaaa tatcccggttc acagagaata gtgaacggga tatttttttat			1642
Asp			
tcttaataca agaataaaaa aacaggtagt aaaccataga tttaccacct gattcattca			1702
cataacaata cagcgaactt ccatgaaaaa aaacattcac ctgtagatta agagacagtt			1762
ggaccgagaa tatatgcaaa tctgttagaa tgaaaatgct agtggaatat tcgatgtttt			1822
tacaagcatc gtttaatat tggacagaca atgtgttaact ctcaattgta caattagttt			1882
tcttttaaaga gaaactgctc cgcaagaaaa acctacggaa cagcttccta atgagaatat			1942
taattagaaa gtttttcgat ttggatatga ccgctgtttc ctgtagcaag agttaacgct			2002
aatccagtga cggcaatctg aatagtagaa gggacagcag taacttcaat catagcttct			2062
cccactaatg gagtacctac gctgattaa			2092
<210> 167			
<211> 364			
<212> PRT			
<213> Bacillus licheniformis			
<400> 167			

Met	Ile	Arg	Leu	Ile	Glu	Pro	Tyr	Ile	Thr	Phe	Glu	Glu	Val	Gln	Ala	1	5	10	15
Glu	Leu	Lys	Glu	Ile	Phe	Ser	Ser	Gly	Met	Leu	Thr	Lys	Gly	Pro	Tyr	20	25	30	
Val	Arg	Thr	Phe	Ala	Asp	His	Met	Arg	Gln	Tyr	Val	Ser	Ala	Lys	His	35	40	45	
Ala	Phe	Leu	Thr	Thr	Ser	Ala	Thr	Thr	Ala	Leu	Ser	Met	Cys	Leu	Lys	50	55	60	
Ser	Leu	Asn	Val	Gln	Pro	Gly	Asp	Glu	Val	Ile	Val	Ser	Asp	Phe	Ser	65	70	75	80
Phe	Pro	Ala	Thr	Val	Asn	Val	Ile	Glu	Asp	Leu	Gly	Ala	Lys	Pro	Val	85	90	95	
Phe	Ala	Asp	Val	Asp	Leu	Glu	Thr	Phe	Asn	Met	Leu	Pro	Glu	Glu	Leu	100	105	110	
Glu	Ser	Gln	Ile	Thr	Ser	Arg	Thr	Lys	Ala	Val	Leu	Phe	Val	Asp	Ala	115	120	125	
Leu	Gly	Asn	Pro	Thr	Gly	Ile	Thr	Asn	Ile	Lys	Gln	Ile	Cys	Lys	Glu	130	135	140	
Tyr	Gly	Leu	Pro	Leu	Val	Asp	Asp	Ala	Ala	Cys	Ala	Ile	Gly	Ser	Ser	145	150	155	160
Glu	Tyr	Gly	Cys	Lys	Ser	Gly	Lys	Ile	Ala	Asp	Leu	Thr	Cys	Phe	Ser	165	170	175	
Phe	His	Pro	Arg	Lys	Leu	Leu	Thr	Thr	Gly	Glu	Gly	Gly	Ala	Ile	Thr	180	185	190	
Thr	Asp	Arg	Glu	Glu	Leu	Lys	Asp	Trp	Leu	Ser	Val	Lys	Leu	Asn	His	195	200	205	
Gly	Ala	Ala	Ile	Ser	Asp	Gly	Lys	Leu	Asp	Phe	Ile	Asp	Phe	Gly	Tyr	210	215	220	

Asn Tyr Arg Leu Ser Asp Ile Gln Ala Ala Leu Gly Ile Lys Gln Leu  
 225 230 235 240

Gln Lys Leu Asp Asp Ile Ile His Arg Arg Asn Leu Gln Gln Lys Ala  
 245 250 255

Tyr Ser Glu Gln Leu Glu Pro Leu Gly Phe Gln Ser Gln Lys Ile Gly  
 260 265 270

Pro Ala Val Val His Asn Ile Gln Ser Ala Val Phe Lys Val Pro Lys  
 275 280 285

Asn Ile Val Arg Asp Glu Leu Ile Gln Tyr Leu Ser Asp Cys His Ile  
 290 295 300

Glu Ser Thr Phe Gly Thr Tyr Cys Leu Ser Gly Thr Pro Tyr Tyr Arg  
 305 310 315 320

Arg Lys Tyr Gln Gln Leu Lys Ser Asn Ser Leu Phe Leu Glu Gln His  
 325 330 335

Thr Ile Thr Leu Pro Cys His Asp Glu Val Asp Leu Asp His Val Val  
 340 345 350

Ser Ala Ile Gln Ser Phe Ile Lys Phe Lys Val Asp  
 355 360

<210> 168  
 <211> 1663  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501) .. (1163)

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 tgggtttccgg ttcacaaac acagctgctc ctcgtatttt tcatcgggct gtcggcagcc 120  
 ggcatttttc cgtgcgccgt cactcttgcc tcgttggttg gaaagccttt tacagaggaa 180  
 atcacgagtc tcttcatttc gtccgcaagt ctgggaggag cgcttctttc attcttgatc 240  
 ggctgggcga ttgatgcaag cgcagccgct gtcttcccgt ttttgctggt cggcggattg 300

gggggcttgc tgctggcgat cagcgcggtg atttttttat ccggcctgca aaaaaacaag	360
cagagtcatt tggatatgta gatttatttag gaagagatta caagcttagt aggatttttt	420
tcagcagccg tttaaaccgt tccatctttg accataatat tgctagaaaa ggttgaagaa	480
cgagaggaac ggtggggaaa atg aag aaa tca aac att gcc tgt atg tat att	533
Met Lys Lys Ser Asn Ile Ala Cys Met Tyr Ile	
1 5 10	
ttt ctt tta tta ata gga gcg ctt gca aat ctc acg acg gaa gag act	581
Phe Leu Leu Leu Ile Gly Ala Leu Ala Asn Leu Thr Thr Glu Glu Thr	
15 20 25	
gcc caa tca tca ggc ggg cag cct gcc gtg att cct gat gaa gcg att	629
Ala Gln Ser Ser Gly Gly Gln Pro Ala Val Ile Pro Asp Glu Ala Ile	
30 35 40	
cgg ctg cgg att ttg gca aac agc gac agc ggg agc gac cag agc gtc	677
Arg Leu Arg Ile Leu Ala Asn Ser Asp Ser Gly Ser Asp Gln Ser Val	
45 50 55	
aaa cgc aaa atc agg gat gag gtc aat aaa caa att acg aaa tgg gtg	725
Lys Arg Lys Ile Arg Asp Glu Val Asn Lys Gln Ile Thr Lys Trp Val	
60 65 70 75	
gaa aac ctg acc tcg gtt gag gaa gcg aga caa gtc atc agg tcg aag	773
Glu Asn Leu Thr Ser Val Glu Glu Ala Arg Gln Val Ile Arg Ser Lys	
80 85 90	
ctg cct gaa atc caa gag gtt gcc atg gat gtc atg aaa cgc gaa aat	821
Leu Pro Glu Ile Gln Glu Val Ala Met Asp Val Met Lys Arg Glu Asn	
95 100 105	
gtt cgg caa tcc gtg tct gtc cgt ttt gat cgt gtt tca ttt ccg aca	869
Val Arg Gln Ser Val Ser Val Arg Phe Asp Arg Val Ser Phe Pro Thr	
110 115 120	
aag cta tac ggc aat atg gtg tat ccg gcc gga gaa tat gag gct gtt	917
Lys Leu Tyr Gly Asn Met Val Tyr Pro Ala Gly Glu Tyr Glu Ala Val	
125 130 135	
tta att aca tta ggc aag gga gag gga gcc aac tgg tgg tgc gtc ctg	965
Leu Ile Thr Leu Gly Lys Gly Glu Gly Ala Asn Trp Trp Cys Val Leu	
140 145 150 155	
ttt ccg cca ctt tgc ttt ctt gat ttt tcc aat ggg gaa gcc gta aag	1013
Phe Pro Pro Leu Cys Phe Leu Asp Phe Ser Asn Gly Glu Ala Val Lys	
160 165 170	
tcg cct gaa gac gaa caa acc gct gcc gga gaa gac cgc cgg gaa gaa	1061
Ser Pro Glu Asp Glu Gln Thr Ala Ala Gly Glu Asp Arg Arg Glu Glu	
175 180 185	
aaa aca gac gcg gcg gat gaa acg gta tct ggc ata gat aaa gat aaa	1109
Lys Thr Asp Ala Ala Asp Glu Thr Val Ser Gly Ile Asp Lys Asp Lys	
190 195 200	

gaa gac aaa gaa gtg aaa ttt ttt ctt gtc gaa tgg att acc ggg ctt 1157  
 Glu Asp Lys Glu Val Lys Phe Phe Leu Val Glu Trp Ile Thr Gly Leu  
 205 210 215  
  
 ttt tct taaaaggacc gccttgcttt cgtgtgcagg gcgggtttttt actgtttgtt 1213  
 Phe Ser  
 220  
  
 ttttcatgat ggttattgaa gcttttgaat atgatataat tttccaaaac ggttcagggg 1273  
  
 aaatactgct tttcggatat acaccttttg cccctttctg atgtgccaat cacattgccg 1333  
  
 gcagaagaga aactgtctta tcaccagtac agcgttcatt tgcataactca ttcaaagcgt 1393  
  
 tggttcctgc taatcaaaaat tgaaaaatga atagccggca ttcttccaaa tcaaaaggta 1453  
  
 tattttactg tcgcccctcat agattggata gagaagttaa aaaacgggggt gaaaagatgt 1513  
  
 tctaccaatt gaggttagcg gaaacgaaag acatgaatgc gatcgaagca tttttaaaaa 1573  
  
 aggcgggggac aagccataag ggtcttgagg aagcgaagag ccagtttatc atgatggaag 1633  
  
 accctcccga tgaaatcgtc gcctgcctcg 1663

<210> 169  
 <211> 221  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 169

Met Lys Lys Ser Asn Ile Ala Cys Met Tyr Ile Phe Leu Leu Leu Ile  
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Gly Ala Leu Ala Asn Leu Thr Thr Glu Glu Thr Ala Gln Ser Ser Gly  
 20 25 30

Gly Gln Pro Ala Val Ile Pro Asp Glu Ala Ile Arg Leu Arg Ile Leu  
 35 40 45

Ala Asn Ser Asp Ser Gly Ser Asp Gln Ser Val Lys Arg Lys Ile Arg  
 50 55 60

Asp Glu Val Asn Lys Gln Ile Thr Lys Trp Val Glu Asn Leu Thr Ser  
 65 70 75 80

Val Glu Glu Ala Arg Gln Val Ile Arg Ser Lys Leu Pro Glu Ile Gln  
 85 90 95

Glu Val Ala Met Asp Val Met Lys Arg Glu Asn Val Arg Gln Ser Val  
 100 105 110

Ser Val Arg Phe Asp Arg Val Ser Phe Pro Thr Lys Leu Tyr Gly Asn  
 115 120 125

Met Val Tyr Pro Ala Gly Glu Tyr Glu Ala Val Leu Ile Thr Leu Gly  
 130 135 140

Lys Gly Glu Gly Ala Asn Trp Trp Cys Val Leu Phe Pro Pro Leu Cys  
 145 150 155 160

Phe Leu Asp Phe Ser Asn Gly Glu Ala Val Lys Ser Pro Glu Asp Glu  
 165 170 175

Gln Thr Ala Ala Gly Glu Asp Arg Arg Glu Glu Lys Thr Asp Ala Ala  
 180 185 190

Asp Glu Thr Val Ser Gly Ile Asp Lys Asp Lys Glu Asp Lys Glu Val  
 195 200 205

Lys Phe Phe Leu Val Glu Trp Ile Thr Gly Leu Phe Ser  
 210 215 220

<210> 170  
 <211> 1351  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(851)

<400> 170  
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 cgttcagcca atatgaaacg catccgatgt ataaacgtaa cgaaatcatt tccgatttga 120  
 aggtcaataa aggccgtgag caaaaaataa accttgtcac atcagaaccg atttcccttt 180  
 tgacgaaaaa aggcgaaaat atcgaatctg ttaaaaaaga aatcaaacag aaagaagata 240  
 tccaggcccc tgtcaaaaaa ggcacagagc ttgggacgct cgttttgaaa aaggatggaa 300  
 aggtgctcgc tgaaagtctt cttgtcgtcg aaaaagatat ggacaaagcg gggatgtgga 360  
 cgatgttcaa gcggacgatg acccactgga cgaagtggag tgaataatgc cgaacggtca 420



ctagttttgt cacggtgaag gaatttataa agtctgaagc gaaacactca ttatccgatt 480

taaaccaagg aggaatgagg atg agc ctc gga atc gat att cac gtc aaa gaa 533  
Met Ser Leu Gly Ile Asp Ile His Val Lys Glu  
1 5 10

tcc gta tta tgc att cgg ttg aca ggt gaa ctc gat cac cat aca gca 581  
Ser Val Leu Cys Ile Arg Leu Thr Gly Glu Leu Asp His His Thr Ala  
15 20 25

gaa acc ttg aga aaa caa gtc agt gac cat ctg gaa caa acc gac att 629  
Glu Thr Leu Arg Lys Gln Val Ser Asp His Leu Glu Gln Thr Asp Ile  
30 35 40

cgc cat att gtc atg aat ctt gca gac ctt tcg ttt atg gac agt tca 677  
Arg His Ile Val Met Asn Leu Ala Asp Leu Ser Phe Met Asp Ser Ser  
45 50 55

ggg ctt ggc gtc gtg ctc ggc aga tat aag gag att aag cag ctc ggc 725  
Gly Leu Gly Val Val Leu Gly Arg Tyr Lys Glu Ile Lys Gln Leu Gly  
60 65 70 75

gga gaa atg atc gtc tgc gcc att tcc cct gct gtc aaa cgt tta ttt 773  
Gly Glu Met Ile Val Cys Ala Ile Ser Pro Ala Val Lys Arg Leu Phe  
80 85 90

gat atg tcc ggg ctg ttt aaa atc att cgc ctt gag caa tca gag cag 821  
Asp Met Ser Gly Leu Phe Lys Ile Ile Arg Leu Glu Gln Ser Glu Gln  
95 100 105

cgt gca ctt gaa acg ttg ggg gtg gcg tca tgaaaaatga aatgaacatt 871  
Arg Ala Leu Glu Thr Leu Gly Val Ala Ser  
110 115

cagtttacag cgctcagcca aaatgaatcg tttgcacggg tgacagtcgc tgcttttatc 931

gctcagcttg acccgacgat ggatgaactg accgaaatta aaacggtcgt atccgaagcg 991

gtcacaaaacg cgatcattca cggttatgaa aactcagggc agggaaacgt atatatttcc 1051

gtcactctcg aggaccatat tgtctattta acgatccgcg acgaaggagt cggcatccct 1111

aatcttgaag aagcgcgccca gcccctgttc acgacaaaagc ctgaactcga gcggtcggga 1171

atgggcttta cgatcatgga aaatttcatg gatgatattt cgatcgactc ctcacctgag 1231

atgggaacca caatacactt aacaaagcac ttatcaaaaa gcaaagcgct ttgcaattaa 1291

gggagatttg ttatggatgt ggagggtaaa aaagaaaacc agaacactca gcttaaagac 1351

<210> 171

<211> 117

<212> PRT

<213> Bacillus licheniformis

<400> 171

Met Ser Leu Gly Ile Asp Ile His Val Lys Glu Ser Val Leu Cys Ile  
 1 5 10 15

Arg Leu Thr Gly Glu Leu Asp His His Thr Ala Glu Thr Leu Arg Lys  
 20 25 30

Gln Val Ser Asp His Leu Glu Gln Thr Asp Ile Arg His Ile Val Met  
 35 40 45

Asn Leu Ala Asp Leu Ser Phe Met Asp Ser Ser Gly Leu Gly Val Val  
 50 55 60

Leu Gly Arg Tyr Lys Glu Ile Lys Gln Leu Gly Gly Glu Met Ile Val  
 65 70 75 80

Cys Ala Ile Ser Pro Ala Val Lys Arg Leu Phe Asp Met Ser Gly Leu  
 85 90 95

Phe Lys Ile Ile Arg Leu Glu Gln Ser Glu Gln Arg Ala Leu Glu Thr  
 100 105 110

Leu Gly Val Ala Ser  
 115

<210> 172  
 <211> 1438  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(938)

<400> 172  
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 cgaacggtca ctagttttgt cacggtgaag gaatttataa agtctgaagc gaaacactca 120  
 ttatccgatt taaaccaagg aggaatgagg atgagcctcg gaatcgatat tcacgtcaaa 180  
 gaatccgtat tatgcattcg gttgacaggt gaactcgatc accatacagc agaaaccttg 240  
 agaaaacaag tcagtgacca tctggaacaa accgacattc gccatattgt catgaatctt 300  
 gcagaccttt cgtttatgga cagttcaggg cttggcgctcg tgctcggcag atataaggag 360  
 attaagcagc tcggcggaga aatgatcgtc tgcgccattt cccctgctgt caaacgttta 420

tttgatatgt ccgggctggt taaaatcatt cgccttgagc aatcagagca gcgtgcactt	480
gaaacgttgg ggggtggcgtc atg aaa aat gaa atg aac att cag ttt aca gcg	533
Met Lys Asn Glu Met Asn Ile Gln Phe Thr Ala	
1 5 10	
ctc agc caa aat gaa tcg ttt gca cgg gtg aca gtc gct gct ttt atc	581
Leu Ser Gln Asn Glu Ser Phe Ala Arg Val Thr Val Ala Ala Phe Ile	
15 20 25	
gct cag ctt gac ccg acg atg gat gaa ctg acc gaa att aaa acg gtc	629
Ala Gln Leu Asp Pro Thr Met Asp Glu Leu Thr Glu Ile Lys Thr Val	
30 35 40	
gta tcc gaa gcg gtc aca aac gcg atc att cac ggt tat gaa aac tca	677
Val Ser Glu Ala Val Thr Asn Ala Ile Ile His Gly Tyr Glu Asn Ser	
45 50 55	
ggg cag gga aac gta tat att tcc gtc act ctc gag gac cat att gtc	725
Gly Gln Gly Asn Val Tyr Ile Ser Val Thr Leu Glu Asp His Ile Val	
60 65 70 75	
tat tta acg atc cgc gac gaa gga gtc ggc atc cct aat ctt gaa gaa	773
Tyr Leu Thr Ile Arg Asp Glu Gly Val Gly Ile Pro Asn Leu Glu Glu	
80 85 90	
gcg cgc cag ccc ctg ttc acg aca aag cct gaa ctc gag cgg tcg gga	821
Ala Arg Gln Pro Leu Phe Thr Thr Lys Pro Glu Leu Glu Arg Ser Gly	
95 100 105	
atg ggc ttt acg atc atg gaa aat ttc atg gat gat att tcg atc gac	869
Met Gly Phe Thr Ile Met Glu Asn Phe Met Asp Asp Ile Ser Ile Asp	
110 115 120	
tcc tca cct gag atg gga acc aca ata cac tta aca aag cac tta tca	917
Ser Ser Pro Glu Met Gly Thr Thr Ile His Leu Thr Lys His Leu Ser	
125 130 135	
aaa agc aaa gcg ctt tgc aat taaggagat ttgttatgga tgtggaggtt	968
Lys Ser Lys Ala Leu Cys Asn	
140 145	
aaaaaagaaa accagaacac tcagcttaaa gaccatgaag tgaaagaact gattaaaaaac	1028
agccagaacg gcgatcaaaa agcaaggac ctccatcatag aaaaaaacat gcgtcttggt	1088
tggtctgtcg ttcagcgttt tttgaacaga ggctatgagc ctgacgacct ctttcaaadc	1148
ggctgcatcg gcctcttgaa gtcggtggac aaattcgatc tttcctatga cgttcggttt	1208
tccacctacg ccgttccgat gattatcggc gagattcagc ggtttatcag agatgacgga	1268
accgtcaaag tgagccgctc gctgaaagaa ctcggaacaa aaatccggcg ggcgaaagac	1328
gagctttcca agtcaaacgg ccggattccg accgttcagg aaatcgccga ttatctcgaa	1388

atcagttcag aagaggtcgt gatggcccag gaagcgggtcc gctctccctc

1438

<210> 173  
<211> 146  
<212> PRT  
<213> Bacillus licheniformis

<400> 173

Met Lys Asn Glu Met Asn Ile Gln Phe Thr Ala Leu Ser Gln Asn Glu  
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Ser Phe Ala Arg Val Thr Val Ala Ala Phe Ile Ala Gln Leu Asp Pro  
20 25 30

Thr Met Asp Glu Leu Thr Glu Ile Lys Thr Val Val Ser Glu Ala Val  
35 40 45

Thr Asn Ala Ile Ile His Gly Tyr Glu Asn Ser Gly Gln Gly Asn Val  
50 55 60

Tyr Ile Ser Val Thr Leu Glu Asp His Ile Val Tyr Leu Thr Ile Arg  
65 70 75 80

Asp Glu Gly Val Gly Ile Pro Asn Leu Glu Glu Ala Arg Gln Pro Leu  
85 90 95

Phe Thr Thr Lys Pro Glu Leu Glu Arg Ser Gly Met Gly Phe Thr Ile  
100 105 110

Met Glu Asn Phe Met Asp Asp Ile Ser Ile Asp Ser Ser Pro Glu Met  
115 120 125

Gly Thr Thr Ile His Leu Thr Lys His Leu Ser Lys Ser Lys Ala Leu  
130 135 140

Cys Asn  
145

<210> 174  
<211> 5482  
<212> DNA  
<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(4982)

<400> 174

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ccatgaagag cctgacgctt caagtcgatc cgaataatct cctttactgg attcagatcg      120
gacgcggcgc caataaagaa gcgcttgaga cggtccgtaa gctggaaaac aatgcacaga      180
tcatgttggc acttatgaaa tacacagatg acattaaagc cgatgataaa ttgtccagtg      240
atgagcggca gaaacagctg gatccgctcg aaaaagaact tgaagaattg aagcggacag      300
cggatgaaca gaaagccaaa actgaagaaa accagcaggc aaacaccgag caaaaccagg      360
cggacgtaga ggccgcaaag gctgaaacgg agaaggccga gaaggaacag gcgaaaaaag      420
aaaataaaga aaaggaagac aaaaagaaaa aagatgacaa ataaaagcga aaacacctgt      480
tggtggcagg aggcggagaa atg agt ctg tta tgg att ttt tat cat aaa aac      533
                Met Ser Leu Leu Trp Ile Phe Tyr His Lys Asn
                1             5             10

tat caa aaa ata aaa ctg gat gat cag aac agc cgc acg ctc acc atc      581
Tyr Gln Lys Ile Lys Leu Asp Asp Gln Asn Ser Arg Thr Leu Thr Ile
                15             20             25

ggg ccg gat ttg aaa cat tct gtc acg att aag cat ttt tca ttt gaa      629
Gly Pro Asp Leu Lys His Ser Val Thr Ile Lys His Phe Ser Phe Glu
                30             35             40

aaa ggc ccg gtg aca ctg gaa aag cag aag gac tca gac gct ttg aac      677
Lys Gly Pro Val Thr Leu Glu Lys Gln Lys Asp Ser Asp Ala Leu Asn
                45             50             55

gtg cag ctg gga ggg gag acg gtc tct tct tta aag ctt ggc gga aag      725
Val Gln Leu Gly Gly Glu Thr Val Ser Ser Leu Lys Leu Gly Gly Lys
                60             65             70             75

gcg tcc gtc caa agc ggc gct gaa cag ctg acg ctc ttt tta gcc gaa      773
Ala Ser Val Gln Ser Gly Ala Glu Gln Leu Thr Leu Phe Leu Ala Glu
                80             85             90

gaa gcc gac agc gtt cct gcc tac tat ttg gga gag aga cag gaa atc      821
Glu Ala Asp Ser Val Pro Ala Tyr Tyr Leu Gly Glu Arg Gln Glu Ile
                95             100             105

gtc att tct tcc ctc gat caa gaa gcg gat gtt tat ttc aat gaa acg      869
Val Ile Ser Ser Leu Asp Gln Glu Ala Asp Val Tyr Phe Asn Glu Thr
                110             115             120

gat tca ttc ttt gga gaa aaa ggt acg ttc tct ttc atc cgc ctc gac      917
Asp Ser Phe Phe Gly Glu Lys Gly Thr Phe Ser Phe Ile Arg Leu Asp
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ggg caa tgg aat gtc ctg ccg aat gac gcg aaa att tat ttg aac gga      965
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agc tcc gag aca aaa aat aaa tat ccg caa tac cgc agg ccg ccg aga Ser Ser Glu Thr Lys Asn Lys Tyr Pro Gln Tyr Arg Arg Pro Pro Arg 205 210 215																1157
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ttc cat ttt cct aca ttt gag aga atg aaa tat tta aca aag gag atc Phe His Phe Pro Thr Phe Glu Arg Met Lys Tyr Leu Thr Lys Glu Ile 335 340 345																1541
agc gga cga att tgg gaa aaa tcg att gaa agc gcc gat ttt ctg caa Ser Gly Arg Ile Trp Glu Lys Ser Ile Glu Ser Ala Asp Phe Leu Gln 350 355 360																1589
atc cgc ctt gga acg gga aat gtt gca tct tcg tac caa atc aat ttg Ile Arg Leu Gly Thr Gly Asn Val Ala Ser Ser Tyr Gln Ile Asn Leu																1637

365	370	375	
aac ggc gga gat ttg gcc aac cgc gat aca gac cat ctc ctt gaa caa			1685
Asn Gly Gly Asp Leu Ala Asn Arg Asp Thr Asp His Leu Leu Glu Gln			
380	385	390	395
acg caa aaa atg gaa gag gtc tac aga gag ctg aaa aat gcg ccg atc			1733
Thr Gln Lys Met Glu Glu Val Tyr Arg Glu Leu Lys Asn Ala Pro Ile			
	400	405	410
act gtg aat ctt gcc gaa ggc ccg atg ggc gtc gtc gga aaa ttg tcc			1781
Thr Val Asn Leu Ala Glu Gly Pro Met Gly Val Val Gly Lys Leu Ser			
	415	420	425
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Val Val Lys Asn Glu Ile His Gln Leu Val Gly Gln Leu Ala Phe Phe			
	430	435	440
cac agc tat cat gac ttg cgc ttt gtc ttt att ttt gac gaa gcc gag			1877
His Ser Tyr His Asp Leu Arg Phe Val Phe Ile Phe Asp Glu Ala Glu			
	445	450	455
tat caa gaa tgg gaa tgg atg aag tgg ctc ccg cat ttt cag atg cct			1925
Tyr Gln Glu Trp Glu Trp Met Lys Trp Leu Pro His Phe Gln Met Pro			
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cat att tat gcg aaa ggg ttt att tac aac gaa cag acg aga gat cag			1973
His Ile Tyr Ala Lys Gly Phe Ile Tyr Asn Glu Gln Thr Arg Asp Gln			
	480	485	490
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Leu Leu Ser Ser Ile Tyr Glu Ile Leu Arg Glu Arg Asp Leu Asp Glu			
	495	500	505
aac aaa aag aag act ttg ttt aag ccg cac ttt gtg ttt atc atc aca			2069
Asn Lys Lys Lys Thr Leu Phe Lys Pro His Phe Val Phe Ile Ile Thr			
	510	515	520
aat cag cag ctc atc gca gaa cac gtc att tta gaa tat ttg gaa ggc			2117
Asn Gln Gln Leu Ile Ala Glu His Val Ile Leu Glu Tyr Leu Glu Gly			
	525	530	535
aag cag aaa cac ctc gga gtg tcg aca atc gtg gcg gca gag aca aaa			2165
Lys Gln Lys His Leu Gly Val Ser Thr Ile Val Ala Ala Glu Thr Lys			
540	545	550	555
gaa agc ctg tcc gaa aac att cat acc ctt gtt cgt tat att act gaa			2213
Glu Ser Leu Ser Glu Asn Ile His Thr Leu Val Arg Tyr Ile Thr Glu			
	560	565	570
cag gaa ggc gac att ctg atc aag caa aag aaa gcc gtc cag atc ccg			2261
Gln Glu Gly Asp Ile Leu Ile Lys Gln Lys Lys Ala Val Gln Ile Pro			
	575	580	585
ttt cag ctg gat cac cac aac agg gaa gac aac gaa cag ttt tcc ccg			2309
Phe Gln Leu Asp His His Asn Arg Glu Asp Asn Glu Gln Phe Ser Arg			
	590	595	600

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ggc tcg ggt aaa agt gaa ttt ttg cag act tat att ttg tct ttg gca Gly Ser Gly Lys Ser Glu Phe Leu Gln Thr Tyr Ile Leu Ser Leu Ala 685 690 695	2597
gtt cac ttt cac ccg cat gaa gtc gca ttt ttg cta atc gac tac aaa Val His Phe His Pro His Glu Val Ala Phe Leu Leu Ile Asp Tyr Lys 700 705 710 715	2645
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acg att act aac att gaa ggc agc aag aac ttc agc aac cgg gcg ctt Thr Ile Thr Asn Ile Glu Gly Ser Lys Asn Phe Ser Asn Arg Ala Leu 735 740 745	2741
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gcg gca agg atc ggg cga agc ctc ggg gtg cac tta atc ttg gcg acg Ala Ala Arg Ile Gly Arg Ser Leu Gly Val His Leu Ile Leu Ala Thr 815 820 825	2981



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860 865 870 875	
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895 900 905	
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Asp Arg Ala Ala Lys Lys Glu Ala Val Thr Glu Ile Ser Ala Val Val	
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Ser Pro Trp Leu Pro Pro Leu Glu Glu Arg Ile Pro Lys Thr Arg Tyr	
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Pro Ser Glu Glu Ala Asp Ala Phe Asn Phe Ala Tyr Ile Asp Glu Pro	
975 980 985	
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Glu Lys Gln Ser Gln Glu Pro Ile Ser Tyr Arg Met Met Glu Asp Gly	
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Ile	Glu	His	Arg	Lys	Asn	Leu	Phe	Arg	Ala	Lys	Glu	Ile	Ser	His	
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Phe	Ile	Thr	Val	Asp	Asn	Phe	Asp	Ile	Ile	Lys	Asp	Glu	Met	His	
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Glu	Leu	Glu	Ser	Glu	Phe	Ile	Gln	Phe	Ser	Arg	Asp	Gly	Gln	Ser	
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Asp	Ile	Glu	Leu	Phe	Glu	Gly	Ile	Lys	Ala	Asp	Ile	Gln	Ala	Ile	
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Ala	Glu	Arg	Ser	Glu	Gly	Met	Arg	Lys	Pro	Ala	Pro	Val	Pro	Met	
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Leu	Pro	Leu	Glu	Leu	Ser	Val	Thr	Gln	Phe	Val	Arg	Asp	Tyr	Pro	
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His Ser Val Thr Ile Lys His Phe Ser Phe Glu Lys Gly Pro Val Thr  
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Glu Thr Val Ser Ser Leu Lys Leu Gly Gly Lys Ala Ser Val Gln Ser  
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Pro Ala Tyr Tyr Leu Gly Glu Arg Gln Glu Ile Val Ile Ser Ser Leu  
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Glu Lys Gly Thr Phe Ser Phe Ile Arg Leu Asp Gly Gln Trp Asn Val  
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Pro Val Ser Val Gln Asn Gly Asp Glu Ile Ala Phe Gly Leu Asn Ile  
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Leu Arg Ile Val Glu Asp Asp Leu Leu Glu Ile Glu Gly Phe Gly Lys  
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Phe Asp Thr Ser Leu Glu Asn Ile Leu Lys Pro Ser Ser Glu Thr Lys  
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Ile His Gln Leu Val Gly Gln Leu Ala Phe Phe His Ser Tyr His Asp  
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Tyr Lys Gly Lys Asp Asp Ile Val Tyr Leu Asn Leu His Glu Lys Ala  
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His Gly Pro His Gly Leu Leu Ala Gly Thr Thr Gly Ser Gly Lys Ser  
675 680 685

Glu Phe Leu Gln Thr Tyr Ile Leu Ser Leu Ala Val His Phe His Pro  
690 695 700

His Glu Val Ala Phe Leu Leu Ile Asp Tyr Lys Gly Gly Gly Met Ala  
705 710 715 720

Gln Pro Phe Arg Asn Ile Pro His Leu Leu Gly Thr Ile Thr Asn Ile  
725 730 735

Glu Gly Ser Lys Asn Phe Ser Asn Arg Ala Leu Ala Ser Ile Lys Ser  
740 745 750

Glu Leu Lys Lys Arg Gln Arg Leu Phe Asp Gln Tyr Lys Val Asn His  
755 760 765

Ile Asn Asp Tyr Thr Lys Leu Tyr Lys Gln Lys Lys Ala Lys Thr Ala  
770 775 780

Met Pro His Leu Phe Leu Ile Ser Asp Glu Phe Ala Glu Leu Lys Ser

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Lys	Val	Gln	Asp	Ala	Asn	Asp	Ser	Lys	Glu	Ile	Leu	Lys	Asn	Gly	Asp
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Ala	Ala	Thr	Ile	Thr	Val	Thr	Gly	Arg	Gly	Tyr	Leu	Gln	Val	Gly	Asn
865					870					875					880
Asn	Glu	Val	Tyr	Glu	Leu	Phe	Gln	Ser	Ala	Trp	Ser	Gly	Ala	Pro	Tyr
				885					890					895	
Met	Glu	Asp	Gly	Tyr	Gly	Thr	Glu	Asp	Glu	Val	Ala	Ile	Val	Thr	Asp
			900					905					910		
Thr	Gly	Leu	Ile	Pro	Leu	Ser	Asp	Val	Asp	Ala	Asp	Arg	Ala	Ala	Lys
		915					920					925			
Lys	Glu	Ala	Val	Thr	Glu	Ile	Ser	Ala	Val	Val	Glu	Gln	Ile	Glu	Arg
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Ile	Gln	Ala	Glu	Met	Gly	Ile	Glu	Lys	Leu	Pro	Ser	Pro	Trp	Leu	Pro
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Pro	Leu	Glu	Glu	Arg	Ile	Pro	Lys	Thr	Arg	Tyr	Pro	Ser	Glu	Glu	Ala
				965					970					975	
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			980					985					990		
Glu	Pro	Ile	Ser	Tyr	Arg	Met	Met	Glu	Asp	Gly	Asn	Ile	Gly	Ile	Val
		995					1000					1005			
Gly	Ser	Ser	Gly	Tyr	Gly	Lys	Ser	Leu	Thr	Ala	Thr	Thr	Phe	Met	
	1010					1015					1020				



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Pro	His	Thr	Ala	Asp	Tyr	Phe	Leu	Met	Asp	Gln	Thr	Arg	Lys	Ile
1055						1060					1065			
Glu	Lys	Phe	Met	Val	Arg	Ile	Lys	Ala	Glu	Ile	Glu	His	Arg	Lys
1070						1075					1080			
Asn	Leu	Phe	Arg	Ala	Lys	Glu	Ile	Ser	His	Ile	Lys	Met	Tyr	Asn
1085						1090					1095			
Ala	Leu	Asn	Glu	Glu	Lys	Leu	Pro	Phe	Ile	Phe	Ile	Thr	Val	Asp
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1160						1165					1170			
Glu	Ala	Tyr	Ser	Ile	Ile	Gly	Arg	Pro	Glu	Phe	Ser	Leu	Glu	Pro
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1190						1195					1200			
Gln	Met	Phe	Met	Pro	Val	Glu	Ala	Asp	Asn	Asp	Ile	Glu	Leu	Phe
1205						1210					1215			
Glu	Gly	Ile	Lys	Ala	Asp	Ile	Gln	Ala	Ile	Ala	Glu	Arg	Ser	Glu
1220						1225					1230			

Gly Met	Arg Lys Pro Ala Pro	Val Pro Met Leu Pro	Leu Glu Leu
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Ser Val	Thr Gln Phe Val Arg	Asp Tyr Pro Leu Gln	Pro Glu Arg
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Gly Leu	Ile Pro Met Gly Leu	Asp Glu Glu Thr Val	Glu Pro Val
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Tyr Phe	Asn Leu Glu Lys Asn	Lys His Cys Leu Ile	Met Gly Gln
1280	1285	1290	
Thr Gln	Arg Gly Lys Thr Asn	Val Ile Lys Ile Met	Leu Glu His
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Asp Arg	Gly Leu Ser Gln Tyr	Ala Thr Glu Asp Gln	Ile Ser Tyr
1325	1330	1335	
Leu Glu	Thr Lys Asp Asp Ile	Leu Leu Trp Leu Ala	Glu Thr Glu
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Glu Ile	Cys Arg Thr Arg Glu	Ala Met Tyr Leu Glu	Ala Val Lys
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Gln Gly	Glu Ile Ala Asn Leu	Asp Phe Ser Pro Met	Val Phe Ile
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Val Asp	Gly Ile Ser Arg Phe	Gln Gln Thr Ile Asp	Ala Ser Ile
1385	1390	1395	
Gln Asp	Lys Met Ala Met Phe	Met Lys Ser Tyr Ala	His Leu Gly
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Phe His	Phe Ile Pro Ala Gly	Asn His Ser Glu Phe	Thr Lys Gly
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Tyr Asp	Ser Leu Thr Ser Glu	Val Lys Gln Val Arg	His Ala Met
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 Gln Lys Gln Gly Lys Lys Arg Ile His Leu Lys Phe Glu Leu Tyr Gly  
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 tta atc tgt atc gcc atc tcg att att gcg gtt ttg cag ctt ggc gta 629  
 Leu Ile Cys Ile Ala Ile Ser Ile Ile Ala Val Leu Gln Leu Gly Val  
 30 35 40  
 gca ggg caa acg ttc att tac atg ttc cgc ttt ttc gcc ggt gaa tgg 677  
 Ala Gly Gln Thr Phe Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp

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Phe Ile Leu Cys Leu Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe			
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Trp Lys Lys Lys Thr Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu			
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tactgc atc att gca agc atg ctg ctt ctt tca cat gtc cag ctg ttt			821
Tyr Cys Ile Ile Ala Ser Met Leu Leu Ser His Val Gln Leu Phe			
	95	100	105
cagcat ttg acc gaa agg gga atg gtt cag tct ccg agc gtg atc caa			869
Gln His Leu Thr Glu Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln			
	110	115	120
aat acg tgg gag ctg ttt ctg atg gat gta aaa ggc gag aca gga tcg			917
Asn Thr Trp Glu Leu Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser			
	125	130	135
cct gat ctt gga ggc gga atg att gga gcc ctt tta ttc gcg gcg tca			965
Pro Asp Leu Gly Gly Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser			
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Tyr Phe Leu Phe Ala Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu			
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atc ttg atc ggc ctt ctt ttg att acg gat cgg tcg ctt cag gag acg			1061
Ile Leu Ile Gly Leu Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr			
	175	180	185
ctg atc aaa tgg atg acc ccg gtc gcc tcc ttc atg aaa aac cag tgg			1109
Leu Ile Lys Trp Met Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp			
	190	195	200
caggcc ttt tta gca gat ctt aaa caa ttg aaa aac agc tcg ccg aaa			1157
Gln Ala Phe Leu Ala Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys			
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aagaaa tcc gga aaa aaa caa aag acg cag aga aaa ccg aaa gtg tct			1205
Lys Lys Ser Gly Lys Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser			
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Glu Glu Pro Val Gln Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln			
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Ser Glu Pro Ile Ile Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu			
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gtt caa gct tac gaa gct ccg gcg gct cct gct gaa cct cct gct gag			1349
Val Gln Ala Tyr Glu Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu			
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ctg gat gat ccg aag cac aca ggg cag cag gcg gat aaa aag aat att Leu Asp Asp Pro Lys His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile 320 325 330	1493
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gca gga gcg acc gga agc ggg aaa agc gtc tgt gtc aac ggg atc att Ala Gly Ala Thr Gly Ser Gly Lys Ser Val Cys Val Asn Gly Ile Ile 460 465 470 475	1925
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Leu Leu Ala Pro Val Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu	
510 515 520	
aag aaa gtc gtc aac gaa atg gag cgg cgc tac gaa ttg ttt tct cac	2117
Lys Lys Val Val Asn Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His	
525 530 535	
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Thr Gly Thr Arg Asn Ile Glu Gly Tyr Asn Asp Tyr Ile Lys Arg Met	
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Ile Val Asp Glu Leu Ala Asp Leu Met Met Val Ala Ser Ser Asp Val	
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Glu Asp Ser Ile Thr Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile	
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His Leu Ile Ile Ala Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly	
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Tyr Asp Glu Ala Val Ala Leu Val Val Ser Met Gln Thr Ala Ser Val	
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tcc atg ctg caa agg aga ttc cgc atc ggc tat aca aga gcg gcg ccg	2741

Ser Met Leu Gln Arg Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg  
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 750 755 760  
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Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu Tyr Cys Ile Ile Ala  
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Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln Asn Thr Trp Glu Leu  
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Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser Pro Asp Leu Gly Gly  
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Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu Ile Leu Ile Gly Leu  
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Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr Leu Ile Lys Trp Met  
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Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp Gln Ala Phe Leu Ala  
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Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys Lys Lys Ser Gly Lys  
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Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser Glu Glu Pro Val Gln  
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Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln Ser Glu Pro Ile Ile  
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Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu Val Gln Ala Tyr Glu  
260 265 270

Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu Pro Glu Ile Gly Glu  
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Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu Leu Asp Asp Pro Lys  
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His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile Tyr Asp Asn Ala Arg  
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Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val Lys Ala Lys Val Thr  
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Gln Val His Leu Gly Pro Ala Val Thr Lys Tyr Glu Val Tyr Pro Asp  
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Val Gly Val Lys Val Ser Lys Ile Val Asn Leu Ser Asp Asp Leu Ala  
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Arg Ala Lys Pro His Glu Val Lys Met Met Met Ile Asp Pro Lys Met  
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Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu Lys Lys Val Val Asn  
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Ala Asp Leu Met Met Val Ala Ser Ser Asp Val Glu Asp Ser Ile Thr  
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Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile His Leu Ile Ile Ala  
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Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro Leu Arg Val Gln Gly  
660 665 670

Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val Val Asp His Val Ile  
675 680 685

Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met Ile Pro Glu Glu Thr  
690 695 700

Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu Tyr Asp Glu Ala Val  
705 710 715 720

Ala Leu Val Val Ser Met Gln Thr Ala Ser Val Ser Met Leu Gln Arg  
725 730 735

Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg Leu Ile Asp Ala Met  
740 745 750

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755

760

765

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&lt;400&gt; 178

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 Glu Asp Ile Glu Lys Leu Asn Val Ser Gln Thr Gln Arg Asp Ile Ala  
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aac cgg atg ctg gcc atg ccg tcc gga tat aga tac ggt tca atc tca 629  
 Asn Arg Met Leu Ala Met Pro Ser Gly Tyr Arg Tyr Gly Ser Ile Ser  
 30 35 40

gaa ctg tta ttt gag ctg aga ttc aga gag cat acc gtc aaa tcg gcc 677  
 Glu Leu Leu Phe Glu Leu Arg Phe Arg Glu His Thr Val Lys Ser Ala  
 45 50 55

aga gag ctg atc aac agc gga gcg aag ttt gcc acc ttt tca aag aca 725  
 Arg Glu Leu Ile Asn Ser Gly Ala Lys Phe Ala Thr Phe Ser Lys Thr  
 60 65 70 75

tac ggg aat gaa gag ttt tgg agg gtg acg cct gag ggg gct ttg gag 773  
 Tyr Gly Asn Glu Glu Phe Trp Arg Val Thr Pro Glu Gly Ala Leu Glu  
 80 85 90

ttg aag tac agg gca ccg gct tca aag gcg att cga aat att ttt gaa	821
Leu Lys Tyr Arg Ala Pro Ala Ser Lys Ala Ile Arg Asn Ile Phe Glu	
95 100 105	
agc ggc cct tct tat gct ttt gag tgc gcg act gcg att gtc atc att	869
Ser Gly Pro Ser Tyr Ala Phe Glu Cys Ala Thr Ala Ile Val Ile Ile	
110 115 120	
ttt tat atg gcg ctt ctc aaa acg atc ggc gac cag aca ttt gac cgg	917
Phe Tyr Met Ala Leu Leu Lys Thr Ile Gly Asp Gln Thr Phe Asp Arg	
125 130 135	
aat tat caa agg atc att tta tac gat tgg cac tat gag cgg ctg ccg	965
Asn Tyr Gln Arg Ile Ile Leu Tyr Asp Trp His Tyr Glu Arg Leu Pro	
140 145 150 155	
atc tat acg gat aaa gga aac gac tac ctt ccg gga gac tgc ctg tat	1013
Ile Tyr Thr Asp Lys Gly Asn Asp Tyr Leu Pro Gly Asp Cys Leu Tyr	
160 165 170	
ttc aag aac cct gaa ttc gat ccc tca aga ccg cag tgg cgc gga gaa	1061
Phe Lys Asn Pro Glu Phe Asp Pro Ser Arg Pro Gln Trp Arg Gly Glu	
175 180 185	
aat gct att tta ctt gaa aat aat ctc tat gcg gca cac ggc ctg ggg	1109
Asn Ala Ile Leu Leu Glu Asn Asn Leu Tyr Ala Ala His Gly Leu Gly	
190 195 200	
atc tta agc ggc gaa aca atc att gaa aaa ctg aac ggg ctg aga aag	1157
Ile Leu Ser Gly Glu Thr Ile Ile Glu Lys Leu Asn Gly Leu Arg Lys	
205 210 215	
cct cat gca cag acg tcc gcc tat ctg ctt tcc caa gtg acg cgg gtt	1205
Pro His Ala Gln Thr Ser Ala Tyr Leu Leu Ser Gln Val Thr Arg Val	
220 225 230 235	
gat att ccg gca tta att caa atg atc aga tagcacatcg gccggcacaa	1255
Asp Ile Pro Ala Leu Ile Gln Met Ile Arg	
240 245	
gctgatccat cagctccttc accgtcgttt gctcgacggg gccccgcacg ctctgtccgg 1315	
cccacaatga catgttatcc gtattcccgt caagcttcgc ctgttttctc atcggttgcg 1375	
tcagcgtggt ttgcagagga taaggcagcg cttcagcttc ttcttggcgt ctgtcttcca 1435	
tccactgatt gacgatgcct cttgccggct tccccgagaa caaacgggtc aggcttgtgt 1495	
cggtttcaac cgcttcgaac aatttttggt tgtaggcagg gtgtgttccg ctttcttcgc 1555	
acgtcaaaaa agcgggtaccg atttgaacgc cctgtgcgcc gagggcaaaa gctgcagcaa 1615	
cacctctttt gtcaaaaatg ccgcccgtg cgataactgg aaccgacaca tgatctgccg 1675	
cttggggaat taaagccatc gagccgacag caggctctcc cttcgttttc aagaaggctc 1735	

<210> 179  
 <211> 245  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 179

Met Ile Ser Val Ser Gly Tyr Arg Leu Arg Pro Glu Asp Ile Glu Lys  
 1 5 10 15

Leu Asn Val Ser Gln Thr Gln Arg Asp Ile Ala Asn Arg Met Leu Ala  
 20 25 30

Met Pro Ser Gly Tyr Arg Tyr Gly Ser Ile Ser Glu Leu Leu Phe Glu  
 35 40 45

Leu Arg Phe Arg Glu His Thr Val Lys Ser Ala Arg Glu Leu Ile Asn  
 50 55 60

Ser Gly Ala Lys Phe Ala Thr Phe Ser Lys Thr Tyr Gly Asn Glu Glu  
 65 70 75 80

Phe Trp Arg Val Thr Pro Glu Gly Ala Leu Glu Leu Lys Tyr Arg Ala  
 85 90 95

Pro Ala Ser Lys Ala Ile Arg Asn Ile Phe Glu Ser Gly Pro Ser Tyr  
 100 105 110

Ala Phe Glu Cys Ala Thr Ala Ile Val Ile Ile Phe Tyr Met Ala Leu  
 115 120 125

Leu Lys Thr Ile Gly Asp Gln Thr Phe Asp Arg Asn Tyr Gln Arg Ile  
 130 135 140

Ile Leu Tyr Asp Trp His Tyr Glu Arg Leu Pro Ile Tyr Thr Asp Lys  
 145 150 155 160

Gly Asn Asp Tyr Leu Pro Gly Asp Cys Leu Tyr Phe Lys Asn Pro Glu  
 165 170 175

Phe Asp Pro Ser Arg Pro Gln Trp Arg Gly Glu Asn Ala Ile Leu Leu  
 180 185 190

Glu Asn Asn Leu Tyr Ala Ala His Gly Leu Gly Ile Leu Ser Gly Glu

195

200

205

Thr Ile Ile Glu Lys Leu Asn Gly Leu Arg Lys Pro His Ala Gln Thr  
 210 215 220

Ser Ala Tyr Leu Leu Ser Gln Val Thr Arg Val Asp Ile Pro Ala Leu  
 225 230 235 240

Ile Gln Met Ile Arg  
 245

<210> 180  
 <211> 1405  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(905)

<400> 180  
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 aatggaatga acaatgcgaa acgccaagga aacggcgcg gatatatattga aaatgatcag 120  
 cacataactca ctgaggcgga acgccaaaac aacaaaaaac ggaaaaccaa tcaataaata 180  
 cgaaagatcc ttcatgaata tcttaggagg ttaaaacatt gacaaataaa aacgacggca 240  
 aagatatgcg caaaaacgca ccgaaaggag ctgagccggg gcagccagag cctttgagcg 300  
 gaagcaaaaa agtaaaaaac cggaaccata caagacaaaa acacaattcc agtcacgata 360  
 tgtaacattt tttccgcgcc tttcacggcg cggttttttt ccttaccgcg cgtcaccctg 420  
 aggcgttgct caccctcctt cacatgaatt caaagggtgtg cataatctaa tggttaaggct 480  
 aggtatggag gaatgctcca atg aca aat aca aaa cgt ttc gat tcc gca gat 533  
 Met Thr Asn Thr Lys Arg Phe Asp Ser Ala Asp  
 1 5 10  
 ttt gat aaa gaa tgg atg aaa cag ttt gtt gac gac cct ttt ctc ctc 581  
 Phe Asp Lys Glu Trp Met Lys Gln Phe Val Asp Asp Pro Phe Leu Leu  
 15 20 25  
 tat gat gaa act tta ccg att gac ctt tat gaa acg agc act gaa tat 629  
 Tyr Asp Glu Thr Leu Pro Ile Asp Leu Tyr Glu Thr Ser Thr Glu Tyr  
 30 35 40  
 ata att gaa gca gat tta agc cac ttg aat gtc cgg cat ctt gac ttg 677  
 Ile Ile Glu Ala Asp Leu Ser His Leu Asn Val Arg His Leu Asp Leu  
 45 50 55

acg ttt tca ggc tac gat ttc aag ctt gca gtt aaa acc gat gag cag 725  
Thr Phe Ser Gly Tyr Asp Phe Lys Leu Ala Val Lys Thr Asp Glu Gln  
60 65 70 75

ctt tac gag aaa tcg ctg atg ctt cct ttc ttt ttg aat gac aaa cag 773  
Leu Tyr Glu Lys Ser Leu Met Leu Pro Phe Phe Leu Asn Asp Lys Gln  
80 85 90

atc gaa gcg gaa tgc gaa aac aac att ctt gca gtt aaa atc aat aaa 821  
Ile Glu Ala Glu Cys Glu Asn Asn Ile Leu Ala Val Lys Ile Asn Lys  
95 100 105

gaa tca agc aaa gat gac att tcg ctt tca atc aat att cct ttt ata 869  
Glu Ser Ser Lys Asp Asp Ile Ser Leu Ser Ile Asn Ile Pro Phe Ile  
110 115 120

tca aac ctg cac aac aag cag aac ccg gac agc gct taaaacactt 915  
Ser Asn Leu His Asn Lys Gln Asn Pro Asp Ser Ala  
125 130 135

gccatccggg ttttttccg ttcgttcgtc aaatatcctc tagcaattct ctatggccga 975

ttagqqaatc gctatacaat agattatggt ctagcatctc ttttgaccag gccggtgtcc 1035

cattttatat tattttttct atgttcttct aaaacgcctt catgtaaaat aggttataga 1095

caaaggaagt atgagagatg ctggaaggat gggttttatg gctgatgctc gcttggatcg 1155

tcatcatgat cgtcctcttg tcaatcggcg gttttttcat gtttcgcaaa tttttaaaaa 1215

ggctgcctaa agaagatggg aaatctgagc tggactggca ggattattat attgaacaga 1275

caagqcattt gtggaatgac gaagaaaaag aactgcttga ggaattggtt tcacccgtac 1335

ccgagctggt tcgcgatgta gcaaaagcaa aaatcgccgg taagatcggg gagcttgcac 1395

tgaaagaaaa	1405
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<210> 181

<211> 135

<212> PRT

<213> Bacillus licheniformis

<400> 181

Met Thr Asn Thr Lys Arg Phe Asp Ser Ala Asp Phe Asp Lys Glu Trp  
1 5 10 15

Met Lys Gln Phe Val Asp Asp Pro Phe Leu Leu Tyr Asp Glu Thr Leu  
20 25 30

Pro Ile Asp Leu Tyr Glu Thr Ser Thr Glu Tyr Ile Ile Glu Ala Asp  
35 40 45

Leu Ser His Leu Asn Val Arg His Leu Asp Leu Thr Phe Ser Gly Tyr  
 50 55 60

Asp Phe Lys Leu Ala Val Lys Thr Asp Glu Gln Leu Tyr Glu Lys Ser  
 65 70 75 80

Leu Met Leu Pro Phe Phe Leu Asn Asp Lys Gln Ile Glu Ala Glu Cys  
 85 90 95

Glu Asn Asn Ile Leu Ala Val Lys Ile Asn Lys Glu Ser Ser Lys Asp  
 100 105 110

Asp Ile Ser Leu Ser Ile Asn Ile Pro Phe Ile Ser Asn Leu His Asn  
 115 120 125

Lys Gln Asn Pro Asp Ser Ala  
 130 135

<210> 182  
 <211> 2155  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1655)

<400> 182  
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 cgatggagaa gacgcaggaa agcgaacgtc cggatattca ctcgtcagtt gccgaaattg 120  
 aagatgtttt gcaaacctca aatgtctatg atcggccatt taccatggaa gaactgaaaa 180  
 acaaattgaa tgagtgcgaa caatattctc agacggagga aggaaagcgt accattctgg 240  
 ctgagtttga atctaaaatc gagaaagttg cgggcattgg tccttttctg acccgtctgc 300  
 acgacatgta cagcagattt acctcggggc gggggacgcc gcgtgaattg ctgctgatgg 360  
 gcggcgcttt gctgtatttc atcgtttctg ttgatgtcat accggattat atttttccga 420  
 tcggctatat cgatgatgcg gcagcgggttc atttcgtttt caaccagctg tcatatataat 480  
 catgatggag catgttcaag atg aaa aga aag cat atc aac att gac atc agt 533  
 Met Lys Arg Lys His Ile Asn Ile Asp Ile Ser  
 1 5 10



ctg ctg ctc att cta ttt tgt ttg ttt atc atc agc ctg ctg gcc gtt Leu Leu Leu Ile Leu Phe Cys Leu Phe Ile Ile Ser Leu Leu Ala Val 15 20 25	581
tac agc ggg tcg ggc cag tat gaa aca cag gac cct ttt tat ttt gcc Tyr Ser Gly Ser Gly Gln Tyr Glu Thr Gln Asp Pro Phe Tyr Phe Ala 30 35 40	629
aaa cgg cag gtc ttt tgg tat ctt gtc ggg ttt ggc gtc atg gcg gga Lys Arg Gln Val Phe Trp Tyr Leu Val Gly Phe Gly Val Met Ala Gly 45 50 55	677
acg gcc tac atc gac tat gag ctg ctt gaa cga ttg gcg ctt cgt tta Thr Ala Tyr Ile Asp Tyr Glu Leu Leu Glu Arg Leu Ala Leu Arg Leu 60 65 70 75	725
ttt gtg gga gcc gtt ttt ctt ctg att ctc gtt cat ttt ttt gga act Phe Val Gly Ala Val Phe Leu Leu Ile Leu Val His Phe Phe Gly Thr 80 85 90	773
tac aaa aac ggt tcg caa agg tgg atc agc ttc ggg gtc atc gaa atc Tyr Lys Asn Gly Ser Gln Arg Trp Ile Ser Phe Gly Val Ile Glu Ile 95 100 105	821
cag cct tca gaa ttt atg aag atc att ttg att ctt ctg ctg gct tcg Gln Pro Ser Glu Phe Met Lys Ile Ile Leu Ile Leu Leu Leu Ala Ser 110 115 120	869
ata ctc aat caa ttt cag cat aaa agg ttc tcc ttc gcc gag agc atc Ile Leu Asn Gln Phe Gln His Lys Arg Phe Ser Phe Ala Glu Ser Ile 125 130 135	917
att ccg acg gga aaa atc atg atg tac acg gtg att ccg ttt ttc ttt Ile Pro Thr Gly Lys Ile Met Met Tyr Thr Val Ile Pro Phe Phe Phe 140 145 150 155	965
ata ttg gtt cag cca gat tta ggg tcc gca ttg gtg att tta tcg atc Ile Leu Val Gln Pro Asp Leu Gly Ser Ala Leu Val Ile Leu Ser Ile 160 165 170	1013
gca ttc acg ttg atg ctg gtc tcg ggg att tcg ggc agg atg atc gtg Ala Phe Thr Leu Met Leu Val Ser Gly Ile Ser Gly Arg Met Ile Val 175 180 185	1061
tcc ctg tca ctt gga ttc atg gca ttg gtt gcc ttt ttg acg tat ttg Ser Leu Ser Leu Gly Phe Met Ala Leu Val Ala Phe Leu Thr Tyr Leu 190 195 200	1109
cac aat cat tac ttt gag ata ttt tca aag att att aag cct cac cag His Asn His Tyr Phe Glu Ile Phe Ser Lys Ile Ile Lys Pro His Gln 205 210 215	1157
ctt gac cgg ata tat ggc tgg ctc agt cct cat gaa cat gcc tct aca Leu Asp Arg Ile Tyr Gly Trp Leu Ser Pro His Glu His Ala Ser Thr 220 225 230 235	1205
tat gga tac cag ctg acg cag gcg tta ttg ggg atc gga tca ggc cag	1253

Tyr Gly Tyr Gln Leu Thr Gln Ala Leu Leu Gly Ile Gly Ser Gly Gln	
240 245 250	
ctg tca ggg agc ggc ttt act caa gga atc caa gtt cag gga ggg aaa	1301
Leu Ser Gly Ser Gly Phe Thr Gln Gly Ile Gln Val Gln Gly Gly Lys	
255 260 265	
att ccg gag gct cat act gat ttt att ttc gcc gtg att ggt gag gaa	1349
Ile Pro Glu Ala His Thr Asp Phe Ile Phe Ala Val Ile Gly Glu Glu	
270 275 280	
ttc ggt ttt ttg ggt gcc gta aca tta gtc tgt ctg tat ttt ctg atg	1397
Phe Gly Phe Leu Gly Ala Val Thr Leu Val Cys Leu Tyr Phe Leu Met	
285 290 295	
atc tac aga atc atc agg att gcg ctt tcg tcc aac agt ctg ttc ggt	1445
Ile Tyr Arg Ile Ile Arg Ile Ala Leu Ser Ser Asn Ser Leu Phe Gly	
300 305 310 315	
ctt tat ata tgt gcg ggg gtt gca ggg ttg att gta ttc caa gtg ttc	1493
Leu Tyr Ile Cys Ala Gly Val Ala Gly Leu Ile Val Phe Gln Val Phe	
320 325 330	
caa aat atc ggg atg acg atc ggg tta atg ccg atc acg ggg ctc gct	1541
Gln Asn Ile Gly Met Thr Ile Gly Leu Met Pro Ile Thr Gly Leu Ala	
335 340 345	
ctt ccg ttt atc agc tat ggc ggc agc gcg ctg ttg acc aac atg atc	1589
Leu Pro Phe Ile Ser Tyr Gly Gly Ser Ala Leu Leu Thr Asn Met Ile	
350 355 360	
gct tta ggt ctc gtt ttc agt gtg aat atc aga tct aaa cat tac atg	1637
Ala Leu Gly Leu Val Phe Ser Val Asn Ile Arg Ser Lys His Tyr Met	
365 370 375	
ttt ggg aat gat tgg gga tgaagttgct caaaatgatt ctttcccatc	1685
Phe Gly Asn Asp Trp Gly	
380 385	
taaagaaact tgattatgta ttgattgccg cggttctggt tttatctgcg tttggcttgc	1745
tgatgggtata cagcgccggc taccctctcg gatatatgaa gtatcatgat ggcagctatt	1805
tttttatgaa gcagctgcaa tggctgctca tcggtttggc ctttttttcg gctgccgcca	1865
ttttcccata caaagcttac agcaaaactca ttcggttttt ggtgaagctt tcttttttaa	1925
tgctgattct cgttttgctg ccgggaatcg ggatggagaa aaacaattcc caaaggtgga	1985
ttcaattcgg ttcgctcatg attcagccgt ctgaggctgt gaagcttgtg atggttattt	2045
atttcgcta tgtgtatgca aaaaagcaga aatacatcgc cgatttcgga aagggcgtca	2105
tgccgccgct gctgattttg gcggctgtgt tttttttgat tttaaaacag	2155

<210> 183

<211> 385  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 183

Met Lys Arg Lys His Ile Asn Ile Asp Ile Ser Leu Leu Leu Ile Leu  
 1 5 10 15

Phe Cys Leu Phe Ile Ile Ser Leu Leu Ala Val Tyr Ser Gly Ser Gly  
 20 25 30

Gln Tyr Glu Thr Gln Asp Pro Phe Tyr Phe Ala Lys Arg Gln Val Phe  
 35 40 45

Trp Tyr Leu Val Gly Phe Gly Val Met Ala Gly Thr Ala Tyr Ile Asp  
 50 55 60

Tyr Glu Leu Leu Glu Arg Leu Ala Leu Arg Leu Phe Val Gly Ala Val  
 65 70 75 80

Phe Leu Leu Ile Leu Val His Phe Phe Gly Thr Tyr Lys Asn Gly Ser  
 85 90 95

Gln Arg Trp Ile Ser Phe Gly Val Ile Glu Ile Gln Pro Ser Glu Phe  
 100 105 110

Met Lys Ile Ile Leu Ile Leu Leu Leu Ala Ser Ile Leu Asn Gln Phe  
 115 120 125

Gln His Lys Arg Phe Ser Phe Ala Glu Ser Ile Ile Pro Thr Gly Lys  
 130 135 140

Ile Met Met Tyr Thr Val Ile Pro Phe Phe Phe Ile Leu Val Gln Pro  
 145 150 155 160

Asp Leu Gly Ser Ala Leu Val Ile Leu Ser Ile Ala Phe Thr Leu Met  
 165 170 175

Leu Val Ser Gly Ile Ser Gly Arg Met Ile Val Ser Leu Ser Leu Gly  
 180 185 190

Phe Met Ala Leu Val Ala Phe Leu Thr Tyr Leu His Asn His Tyr Phe  
 195 200 205

Glu Ile Phe Ser Lys Ile Ile Lys Pro His Gln Leu Asp Arg Ile Tyr  
 210 215 220

Gly Trp Leu Ser Pro His Glu His Ala Ser Thr Tyr Gly Tyr Gln Leu  
 225 230 235 240

Thr Gln Ala Leu Leu Gly Ile Gly Ser Gly Gln Leu Ser Gly Ser Gly  
 245 250 255

Phe Thr Gln Gly Ile Gln Val Gln Gly Gly Lys Ile Pro Glu Ala His  
 260 265 270

Thr Asp Phe Ile Phe Ala Val Ile Gly Glu Glu Phe Gly Phe Leu Gly  
 275 280 285

Ala Val Thr Leu Val Cys Leu Tyr Phe Leu Met Ile Tyr Arg Ile Ile  
 290 295 300

Arg Ile Ala Leu Ser Ser Asn Ser Leu Phe Gly Leu Tyr Ile Cys Ala  
 305 310 315 320

Gly Val Ala Gly Leu Ile Val Phe Gln Val Phe Gln Asn Ile Gly Met  
 325 330 335

Thr Ile Gly Leu Met Pro Ile Thr Gly Leu Ala Leu Pro Phe Ile Ser  
 340 345 350

Tyr Gly Gly Ser Ala Leu Leu Thr Asn Met Ile Ala Leu Gly Leu Val  
 355 360 365

Phe Ser Val Asn Ile Arg Ser Lys His Tyr Met Phe Gly Asn Asp Trp  
 370 375 380

Gly  
 385

<210> 184  
 <211> 2113  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS

<222> (501)..(1613)

<400> 184

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cgacgcggcc gtccgtaagg tgctgacgag ctttacaggt gttaagcaca ggatgcaata      60
cgtcgcgacg atcaaaaaaca gactgtttta caatgacagc aaagcgacaa acattcttgc    120
gacgaaaaaaa gcgctgtccg cctttcaaaa gccggtcatt ttgctggcag gggggcttga    180
ccgcggaaat gaatttgatg aactaaagcc gcatatgtct tttgtaaaaag cggtgatcac    240
tttcggcgag accgcgccga agtttgagaa gctggccgaa gaaatgggaa tacaacaggt    300
taaacgtgtc gataatgttg aacaagcagc aactgcggcg ttcagcctgt cagacgaagg    360
agatgtcatt cttctgtccc cggcctgcgc aagctgggat cagtacaaaa catttgaaga    420
acgtggtgac atgtttgtaa acgccgtgca tatgcttaaa taagggtctg tctcgtaaag    480
atagccctaa gaattagagc ttg ggg tgt tcg gct ttg caa aca aaa aaa acg      533
                  Leu Gly Cys Ser Ala Leu Gln Thr Lys Lys Thr
                  1              5              10

tca ccg gat ttt ttg ctg gtt atc att acg cta ttg ctt tta aca atc      581
Ser Pro Asp Phe Leu Leu Val Ile Ile Thr Leu Leu Leu Leu Thr Ile
                  15              20              25

gga ctg att atg gta tac agc gcc agt gca gta tgg gcg act tac aaa      629
Gly Leu Ile Met Val Tyr Ser Ala Ser Ala Val Trp Ala Thr Tyr Lys
                  30              35              40

tac gac gac tcc ttt ttc ttt gcg aaa cgg cag ctt ttg ttt gcc ggc      677
Tyr Asp Asp Ser Phe Phe Phe Ala Lys Arg Gln Leu Leu Phe Ala Gly
                  45              50              55

atc ggg gtc atc gcc atg ttt ttc atc atg aac gtc gac tac tgg acg      725
Ile Gly Val Ile Ala Met Phe Phe Ile Met Asn Val Asp Tyr Trp Thr
                  60              65              70              75

tgg agg act tat gcg aaa ata ctg atc att gta tgt ttc ttt ctg ctc      773
Trp Arg Thr Tyr Ala Lys Ile Leu Ile Ile Val Cys Phe Phe Leu Leu
                  80              85              90

atc atc gtc ctg gtt ccc ggg atc ggc atg gaa cgg aac ggg tcg agg      821
Ile Ile Val Leu Val Pro Gly Ile Gly Met Glu Arg Asn Gly Ser Arg
                  95              100              105

agc tgg atc gga gtc ggc gct ttc agc att cag ccg tcc gag ttt atg      869
Ser Trp Ile Gly Val Gly Ala Phe Ser Ile Gln Pro Ser Glu Phe Met
                  110              115              120

aaa ctc gcg atg atc gca ttt ttg gcc aag ttt tta tct gaa aag caa      917
Lys Leu Ala Met Ile Ala Phe Leu Ala Lys Phe Leu Ser Glu Lys Gln
                  125              130              135

aag aat att acg tcg ttt aga aaa ggc ttt gtg ccg gcg ctg ggc att      965
Lys Asn Ile Thr Ser Phe Arg Lys Gly Phe Val Pro Ala Leu Gly Ile
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140	145	150	155	
gtc ttt tca gct ttt ctg atc atc atg atg cag cct gac ctc gga aca				1013
Val Phe Ser Ala Phe Leu Ile Ile Met Met Gln Pro Asp Leu Gly Thr				
	160	165	170	
gga acc gtg atg gtc ggc aca tgc atc att atg atc ttt gtc gcg ggg				1061
Gly Thr Val Met Val Gly Thr Cys Ile Ile Met Ile Phe Val Ala Gly				
	175	180	185	
gcg aga att tcg cac ttc gtt ttt ctc ggc ctg atc gga ctg agc ggt				1109
Ala Arg Ile Ser His Phe Val Phe Leu Gly Leu Ile Gly Leu Ser Gly				
	190	195	200	
ttt gtc ggc ctt gtg ctg tcg gcg ccg tac cgg atc aaa agg atc act				1157
Phe Val Gly Leu Val Leu Ser Ala Pro Tyr Arg Ile Lys Arg Ile Thr				
	205	210	215	
tca tac ttg aac cct tgg gag gac cct tta gga agc ggc ttt caa atc				1205
Ser Tyr Leu Asn Pro Trp Glu Asp Pro Leu Gly Ser Gly Phe Gln Ile				
	220	225	230	235
att cag tct ctt tat gcg gtg ggg ccc ggc ggg ctg ttc ggc ctc ggc				1253
Ile Gln Ser Leu Tyr Ala Val Gly Pro Gly Gly Leu Phe Gly Leu Gly				
	240	245	250	
ctc ggc cag agc agg caa aag ttt ttc tat ctg cct gag ccg cag aca				1301
Leu Gly Gln Ser Arg Gln Lys Phe Phe Tyr Leu Pro Glu Pro Gln Thr				
	255	260	265	
gat ttt att ttt gcg att tta tca gag gag ctc ggc ttt atc ggc gga				1349
Asp Phe Ile Phe Ala Ile Leu Ser Glu Glu Leu Gly Phe Ile Gly Gly				
	270	275	280	
tcg ctg att ctt ttg ctc ttc agc gtt cta tta tgg aga ggc atc aga				1397
Ser Leu Ile Leu Leu Leu Phe Ser Val Leu Leu Trp Arg Gly Ile Arg				
	285	290	295	
atc gcg ctc ggt gcg ccc gat tta tac ggc agt ttt gtc gcc gtc ggc				1445
Ile Ala Leu Gly Ala Pro Asp Leu Tyr Gly Ser Phe Val Ala Val Gly				
	300	305	310	315
gtc att tcg atg ata gcg att cag gtt atg atc aat atc gga gtc gtg				1493
Val Ile Ser Met Ile Ala Ile Gln Val Met Ile Asn Ile Gly Val Val				
	320	325	330	
act ggt ttg att cct gtt aca ggc att acg ctt ccg ttt tta agc tat				1541
Thr Gly Leu Ile Pro Val Thr Gly Ile Thr Leu Pro Phe Leu Ser Tyr				
	335	340	345	
ggc ggt tca tca ctg acc ttg atg ctc atg gcg gtc ggc gtg ctg ctg				1589
Gly Gly Ser Ser Leu Thr Leu Met Leu Met Ala Val Gly Val Leu Leu				
	350	355	360	
aat gtc agc agg tat tct aga tac tagattttgg cgataaccct gttgcgagat				1643
Asn Val Ser Arg Tyr Ser Arg Tyr				
	365	370		

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 ggcatcacga agatgttgag tttttatata tcggaaccga aaaaggcctg gagaaaaata 1823  
 tcgtcgagcg ggaagggatc cctttcaaag cgattgaaat tacgggtttt aaaagaaaac 1883  
 tttcatttga aaacgtcaaa accgtcatgc gctttttaa ggggtgtaaaa gaatgcaaag 1943  
 aagaattaaa acggttcaag ccggatgccg tgatcggcac gggcggctac gtgtgcggcc 2003  
 ccgtcgata cgccgcttca aaactgggga ttccgacgat tatccacgaa caaacagcc 2063  
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<400> 185

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Tyr Ser Ala Ser Ala Val Trp Ala Thr Tyr Lys Tyr Asp Asp Ser Phe  
 35 40 45

Phe Phe Ala Lys Arg Gln Leu Leu Phe Ala Gly Ile Gly Val Ile Ala  
 50 55 60

Met Phe Phe Ile Met Asn Val Asp Tyr Trp Thr Trp Arg Thr Tyr Ala  
 65 70 75 80

Lys Ile Leu Ile Ile Val Cys Phe Phe Leu Leu Ile Ile Val Leu Val  
 85 90 95

Pro Gly Ile Gly Met Glu Arg Asn Gly Ser Arg Ser Trp Ile Gly Val  
 100 105 110

Gly Ala Phe Ser Ile Gln Pro Ser Glu Phe Met Lys Leu Ala Met Ile  
 115 120 125

Ala Phe Leu Ala Lys Phe Leu Ser Glu Lys Gln Lys Asn Ile Thr Ser  
130 135 140

Phe Arg Lys Gly Phe Val Pro Ala Leu Gly Ile Val Phe Ser Ala Phe  
145 150 155 160

Leu Ile Ile Met Met Gln Pro Asp Leu Gly Thr Gly Thr Val Met Val  
165 170 175

Gly Thr Cys Ile Ile Met Ile Phe Val Ala Gly Ala Arg Ile Ser His  
180 185 190

Phe Val Phe Leu Gly Leu Ile Gly Leu Ser Gly Phe Val Gly Leu Val  
195 200 205

Leu Ser Ala Pro Tyr Arg Ile Lys Arg Ile Thr Ser Tyr Leu Asn Pro  
210 215 220

Trp Glu Asp Pro Leu Gly Ser Gly Phe Gln Ile Ile Gln Ser Leu Tyr  
225 230 235 240

Ala Val Gly Pro Gly Gly Leu Phe Gly Leu Gly Leu Gly Gln Ser Arg  
245 250 255

Gln Lys Phe Phe Tyr Leu Pro Glu Pro Gln Thr Asp Phe Ile Phe Ala  
260 265 270

Ile Leu Ser Glu Glu Leu Gly Phe Ile Gly Gly Ser Leu Ile Leu Leu  
275 280 285

Leu Phe Ser Val Leu Leu Trp Arg Gly Ile Arg Ile Ala Leu Gly Ala  
290 295 300

Pro Asp Leu Tyr Gly Ser Phe Val Ala Val Gly Val Ile Ser Met Ile  
305 310 315 320

Ala Ile Gln Val Met Ile Asn Ile Gly Val Val Thr Gly Leu Ile Pro  
325 330 335

Val Thr Gly Ile Thr Leu Pro Phe Leu Ser Tyr Gly Gly Ser Ser Leu  
340 345 350

Thr Leu Met Leu Met Ala Val Gly Val Leu Leu Asn Val Ser Arg Tyr



355

360

365

Ser Arg Tyr  
370

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aaggcgacat taaagtggat taccggatgg atttggccaa gctgatgaag aagtcgaaaa 180  
aaacggtaaa gccgggagag gaagtccaag atttgatgtg ggaagagacg cctttcgttc 240  
cggcgttttc ggtaaagtac acagtgaatg acaaacagga acctgttttt ctcgaataga 300  
atatcgggtca aaatgcaagt atcagtcatg aacctttctc ctcggcatac aatgaggaga 360  
aagggtttttt catgtatgcc gaaaaaattt ccctaagctg tcatattgaa ataggacaac 420  
gtcatacact atagtgtcct gtttttgatt gatgaagaag taaaaaattg aaaaggattg 480  
gaagtcgggg aggggatcac ttg gaa aag gtc gat att ttc aag gat atc gct 533  
Leu Glu Lys Val Asp Ile Phe Lys Asp Ile Ala  
1 5 10  
gaa cga aca gga ggc gat ata tac tta ggt gtc gta gga gct gta cgt 581  
Glu Arg Thr Gly Gly Asp Ile Tyr Leu Gly Val Val Gly Ala Val Arg  
15 20 25  
aca gga aaa tct acg ttt atc aaa aaa ttt atg gag cta gtg gtg ctc 629  
Thr Gly Lys Ser Thr Phe Ile Lys Lys Phe Met Glu Leu Val Val Leu  
30 35 40  
ccg aat atc aac aat gaa gca gac cgg gcg cgc gca caa gat gag ctc 677  
Pro Asn Ile Asn Asn Glu Ala Asp Arg Ala Arg Ala Gln Asp Glu Leu  
45 50 55  
ccc caa agt gcc gct ggc aaa acc att atg aca act gaa ccg aag ttt 725  
Pro Gln Ser Ala Ala Gly Lys Thr Ile Met Thr Thr Glu Pro Lys Phe  
60 65 70 75  
gtt ccg aat cag gca atg tca gtt cat gtc agt gac gga ctc gat gtg 773  
Val Pro Asn Gln Ala Met Ser Val His Val Ser Asp Gly Leu Asp Val  
80 85 90

aat ata agg ctt gtc gac tgc gtc ggc tat act gta ccc ggg gca aag	821
Asn Ile Arg Leu Val Asp Cys Val Gly Tyr Thr Val Pro Gly Ala Lys	
95 100 105	
gga tac gag gat gaa aac ggg ccg aga atg atc aat act cct tgg tat	869
Gly Tyr Glu Asp Glu Asn Gly Pro Arg Met Ile Asn Thr Pro Trp Tyr	
110 115 120	
gaa gag ccg att ccg ttt cac gaa gct gcc gaa atc ggc acg aga aaa	917
Glu Glu Pro Ile Pro Phe His Glu Ala Ala Glu Ile Gly Thr Arg Lys	
125 130 135	
gtc atc caa gag cac tcc aca atc ggt gtt gtg att acg act gac ggc	965
Val Ile Gln Glu His Ser Thr Ile Gly Val Val Ile Thr Thr Asp Gly	
140 145 150 155	
acg att gga gaa atc gcc aga cag gat tat gtc gag gct gaa gaa cgg	1013
Thr Ile Gly Glu Ile Ala Arg Gln Asp Tyr Val Glu Ala Glu Glu Arg	
160 165 170	
gtg atc gac gag ttg aaa gag gtt gga aaa ccg ttt atc atg gtc atc	1061
Val Ile Asp Glu Leu Lys Glu Val Gly Lys Pro Phe Ile Met Val Ile	
175 180 185	
aat tcc gta agg ccg tat cat ccg gaa aca gaa gcg ctc agg caa gaa	1109
Asn Ser Val Arg Pro Tyr His Pro Glu Thr Glu Ala Leu Arg Gln Glu	
190 195 200	
ttg atg gaa aag tac gac att ccg gtg ctg gcg atg agc gtt gaa agc	1157
Leu Met Glu Lys Tyr Asp Ile Pro Val Leu Ala Met Ser Val Glu Ser	
205 210 215	
atg agg gaa gcg gac gtt ctg agc gtt ctc aga gaa gcg ctt tac gaa	1205
Met Arg Glu Ala Asp Val Leu Ser Val Leu Arg Glu Ala Leu Tyr Glu	
220 225 230 235	
ttc cct gtg ctc gaa gtc aac gtc aat ctt cca agc tgg gtg atg gta	1253
Phe Pro Val Leu Glu Val Asn Val Asn Leu Pro Ser Trp Val Met Val	
240 245 250	
tta aaa gag aat cat tgg ctc agg gaa aac tat caa gat tcc gtt aaa	1301
Leu Lys Glu Asn His Trp Leu Arg Glu Asn Tyr Gln Asp Ser Val Lys	
255 260 265	
gaa acc gtc aaa gat att aaa aga ctg aga gat gtc gac cgc gtc gtc	1349
Glu Thr Val Lys Asp Ile Lys Arg Leu Arg Asp Val Asp Arg Val Val	
270 275 280	
gga cac ttc agc gaa ttt gat ttc atc gag cgc gca agc ctc gcc gga	1397
Gly His Phe Ser Glu Phe Asp Phe Ile Glu Arg Ala Ser Leu Ala Gly	
285 290 295	
att gaa atg ggc cag ggg atc gcg gaa atc gat tta tac gcg ccg gat	1445
Ile Glu Met Gly Gln Gly Ile Ala Glu Ile Asp Leu Tyr Ala Pro Asp	
300 305 310 315	

tac ctg tac gat gaa att ttg agg gaa gtc gtc ggc gtt gaa atc aga	1493
Tyr Leu Tyr Asp Glu Ile Leu Arg Glu Val Val Gly Val Glu Ile Arg	
320 325 330	
gga aaa gat cac ctc ctt cag ctc atg cag gat ttt gcc cat gcc aag	1541
Gly Lys Asp His Leu Leu Gln Leu Met Gln Asp Phe Ala His Ala Lys	
335 340 345	
acc gaa tat gat caa gtc tca gat gca ttg aaa atg gtg aaa caa acc	1589
Thr Glu Tyr Asp Gln Val Ser Asp Ala Leu Lys Met Val Lys Gln Thr	
350 355 360	
ggc tat gga atc gca gct ccc gca tta acc gat atg agc ctg gat gaa	1637
Gly Tyr Gly Ile Ala Ala Pro Ala Leu Thr Asp Met Ser Leu Asp Glu	
365 370 375	
ccg gaa atc atc agg cag ggt tca aga ttc gga gtc cgg ctg aag gcg	1685
Pro Glu Ile Ile Arg Gln Gly Ser Arg Phe Gly Val Arg Leu Lys Ala	
380 385 390 395	
gtg gcg ccg tcg att cat atg atc aaa gtc gat gtg gaa agc gag ttt	1733
Val Ala Pro Ser Ile His Met Ile Lys Val Asp Val Glu Ser Glu Phe	
400 405 410	
gcg ccg atc atc gga aca gag aag cag agc gaa gag ctt gtc cgc tat	1781
Ala Pro Ile Ile Gly Thr Glu Lys Gln Ser Glu Glu Leu Val Arg Tyr	
415 420 425	
tta atg cag gac ttt gag gac gat ccg ctg tca atc tgg aat tcc gac	1829
Leu Met Gln Asp Phe Glu Asp Asp Pro Leu Ser Ile Trp Asn Ser Asp	
430 435 440	
ata ttc gga aga agc ttg agc tcg atc gtc aga gaa ggg att cag gcg	1877
Ile Phe Gly Arg Ser Leu Ser Ser Ile Val Arg Glu Gly Ile Gln Ala	
445 450 455	
aag ctg tca ctc atg cct gaa aat gcg aga tat aag ctg aag gag acg	1925
Lys Leu Ser Leu Met Pro Glu Asn Ala Arg Tyr Lys Leu Lys Glu Thr	
460 465 470 475	
ctg gag cgc att atc aat gaa ggc tca ggc ggc ttg att gcg atc atc	1973
Leu Glu Arg Ile Ile Asn Glu Gly Ser Gly Gly Leu Ile Ala Ile Ile	
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Leu	
acaggctgaa cggg	2040

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 20 25 30  
 Phe Ile Lys Lys Phe Met Glu Leu Val Val Leu Pro Asn Ile Asn Asn  
 35 40 45  
 Glu Ala Asp Arg Ala Arg Ala Gln Asp Glu Leu Pro Gln Ser Ala Ala  
 50 55 60  
 Gly Lys Thr Ile Met Thr Thr Glu Pro Lys Phe Val Pro Asn Gln Ala  
 65 70 75 80  
 Met Ser Val His Val Ser Asp Gly Leu Asp Val Asn Ile Arg Leu Val  
 85 90 95  
 Asp Cys Val Gly Tyr Thr Val Pro Gly Ala Lys Gly Tyr Glu Asp Glu  
 100 105 110  
 Asn Gly Pro Arg Met Ile Asn Thr Pro Trp Tyr Glu Glu Pro Ile Pro  
 115 120 125  
 Phe His Glu Ala Ala Glu Ile Gly Thr Arg Lys Val Ile Gln Glu His  
 130 135 140  
 Ser Thr Ile Gly Val Val Ile Thr Thr Asp Gly Thr Ile Gly Glu Ile  
 145 150 155 160  
 Ala Arg Gln Asp Tyr Val Glu Ala Glu Glu Arg Val Ile Asp Glu Leu  
 165 170 175  
 Lys Glu Val Gly Lys Pro Phe Ile Met Val Ile Asn Ser Val Arg Pro  
 180 185 190  
 Tyr His Pro Glu Thr Glu Ala Leu Arg Gln Glu Leu Met Glu Lys Tyr  
 195 200 205  
 Asp Ile Pro Val Leu Ala Met Ser Val Glu Ser Met Arg Glu Ala Asp  
 210 215 220

Val Leu Ser Val Leu Arg Glu Ala Leu Tyr Glu Phe Pro Val Leu Glu  
 225 230 235 240

Val Asn Val Asn Leu Pro Ser Trp Val Met Val Leu Lys Glu Asn His  
 245 250 255

Trp Leu Arg Glu Asn Tyr Gln Asp Ser Val Lys Glu Thr Val Lys Asp  
 260 265 270

Ile Lys Arg Leu Arg Asp Val Asp Arg Val Val Gly His Phe Ser Glu  
 275 280 285

Phe Asp Phe Ile Glu Arg Ala Ser Leu Ala Gly Ile Glu Met Gly Gln  
 290 295 300

Gly Ile Ala Glu Ile Asp Leu Tyr Ala Pro Asp Tyr Leu Tyr Asp Glu  
 305 310 315 320

Ile Leu Arg Glu Val Val Gly Val Glu Ile Arg Gly Lys Asp His Leu  
 325 330 335

Leu Gln Leu Met Gln Asp Phe Ala His Ala Lys Thr Glu Tyr Asp Gln  
 340 345 350

Val Ser Asp Ala Leu Lys Met Val Lys Gln Thr Gly Tyr Gly Ile Ala  
 355 360 365

Ala Pro Ala Leu Thr Asp Met Ser Leu Asp Glu Pro Glu Ile Ile Arg  
 370 375 380

Gln Gly Ser Arg Phe Gly Val Arg Leu Lys Ala Val Ala Pro Ser Ile  
 385 390 395 400

His Met Ile Lys Val Asp Val Glu Ser Glu Phe Ala Pro Ile Ile Gly  
 405 410 415

Thr Glu Lys Gln Ser Glu Glu Leu Val Arg Tyr Leu Met Gln Asp Phe  
 420 425 430

Glu Asp Asp Pro Leu Ser Ile Trp Asn Ser Asp Ile Phe Gly Arg Ser  
 435 440 445

Leu Ser Ser Ile Val Arg Glu Gly Ile Gln Ala Lys Leu Ser Leu Met

450	455	460	
Pro Glu Asn Ala Arg Tyr Lys Leu Lys Glu Thr Leu Glu Arg Ile Ile			
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Asn Glu Gly Ser Gly Gly Leu Ile Ala Ile Ile Leu			
	485	490	
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gacgcggcgc caataaagaa gcgcttgaga cggcccgtaa gctggaaaac aatgcacaga			180
tcatgttggc acttatgaaa tacacagatg acattaaagc cgatgataaa ttgtccagtg			240
atgagcggca gaaacagctg gatccgctcg aaaaagaact tgaagaattg aagcggacag			300
cggatgaaca gaaagccaaa actgaagaaa accagcaggc aaacaccgag caaaaccagg			360
cggacgtaga ggccgcaaag gctgaaacgg agaaggccga gaaggaacag gcgaaaaaag			420
aaaataaaga aaaggaagac aaaaagaaaa aagatgacaa ataaaagcga aaacacctgt			480
tggttggcagg aggcggagaa atg agt ctg tta tgg att ttt tat cat aaa aac			533
	Met Ser Leu Leu Trp Ile Phe Tyr His Lys Asn		
	1 5 10		
tat caa aaa ata aaa ctg gat gat cag aac agc cgc acg ctc acc atc			581
Tyr Gln Lys Ile Lys Leu Asp Asp Gln Asn Ser Arg Thr Leu Thr Ile			
	15 20 25		
ggg ccg gat ttg aaa cat tct gtc acg att aag cat ttt tca ttt gaa			629
Gly Pro Asp Leu Lys His Ser Val Thr Ile Lys His Phe Ser Phe Glu			
	30 35 40		
aaa ggc ccg gtg aca ctg gaa aag cag aag gac tca gac gct ttg aac			677
Lys Gly Pro Val Thr Leu Glu Lys Gln Lys Asp Ser Asp Ala Leu Asn			
	45 50 55		
gtg cag ctg gga ggg gag acg gtc tct tct tta aag ctt ggc gga aag			725
Val Gln Leu Gly Gly Glu Thr Val Ser Ser Leu Lys Leu Gly Gly Lys			
	60 65 70 75		

gcg tcc gtc caa agc ggc gct gaa cag ctg acg ctc ttt tta gcc gaa	773
Ala Ser Val Gln Ser Gly Ala Glu Gln Leu Thr Leu Phe Leu Ala Glu	
80 85 90	
gaa gcc gac agc gtt cct gcc tac tat ttg gga gag aga cag gaa atc	821
Glu Ala Asp Ser Val Pro Ala Tyr Tyr Leu Gly Glu Arg Gln Glu Ile	
95 100 105	
gtc att tct tcc ctc gat caa gaa gcg gat gtt tat ttc aat gaa acg	869
Val Ile Ser Ser Leu Asp Gln Ala Asp Val Tyr Phe Asn Glu Thr	
110 115 120	
gat tca ttc ttt gga gaa aaa ggt acg ttc tct ttc atc cgc ctc gac	917
Asp Ser Phe Phe Gly Glu Lys Gly Thr Phe Ser Phe Ile Arg Leu Asp	
125 130 135	
ggg caa tgg aat gtc ctg ccg aat gac gcg aaa att tat ttg aac gga	965
Gly Gln Trp Asn Val Leu Pro Asn Asp Ala Lys Ile Tyr Leu Asn Gly	
140 145 150 155	
gaa gaa gtg tcc gcc cct gtc tcc gtg caa aat gga gac gaa atc gca	1013
Glu Glu Val Ser Ala Pro Val Ser Val Gln Asn Gly Asp Glu Ile Ala	
160 165 170	
ttt gga ctg aat att ctt cgc atc gtt gaa gac gac ctc ttg gaa atc	1061
Phe Gly Leu Asn Ile Leu Arg Ile Val Glu Asp Asp Leu Leu Glu Ile	
175 180 185	
gag gga ttc ggg aag ttt gat acg tct ttg gag aac att ctt aag ccg	1109
Glu Gly Phe Gly Lys Phe Asp Thr Ser Leu Glu Asn Ile Leu Lys Pro	
190 195 200	
agc tcc gag aca aaa aat aaa tat ccg caa tac cgc agg ccg ccg aga	1157
Ser Ser Glu Thr Lys Asn Lys Tyr Pro Gln Tyr Arg Arg Pro Pro Arg	
205 210 215	
atg att tac gac ctg ccg gat gaa aaa gta tcc ttc agc ttc ccg gca	1205
Met Ile Tyr Asp Leu Pro Asp Glu Lys Val Ser Phe Ser Phe Pro Ala	
220 225 230 235	
cag gaa agc gac gga gac aac aga ggc cta tgg ctg atg att ctg cct	1253
Gln Glu Ser Asp Gly Asp Asn Arg Gly Leu Trp Leu Met Ile Leu Pro	
240 245 250	
ccg ctc gtc atg ctg atc gtc atg ggg atc gtg gcg ctc att cag ccg	1301
Pro Leu Val Met Leu Ile Val Met Gly Ile Val Ala Leu Ile Gln Pro	
255 260 265	
cgg ggg atc ttt atc atc gtt tcc ctt gcg atg ttt atg atg acg ctg	1349
Arg Gly Ile Phe Ile Ile Val Ser Leu Ala Met Phe Met Met Thr Leu	
270 275 280	
att acg tca acc gtg cag tac ttc cgc gac aaa aat cag cgt aaa aaa	1397
Ile Thr Ser Thr Val Gln Tyr Phe Arg Asp Lys Asn Gln Arg Lys Lys	
285 290 295	

aga gaa gaa aaa aga gag cgg gtc tat acc ctt tac ctt gaa aac aaa	1445
Arg Glu Glu Lys Arg Glu Arg Val Tyr Thr Leu Tyr Leu Glu Asn Lys	
300 305 310 315	
aag aaa gag ctg cat gaa ctt gca gaa aga caa aag ttc gta ctt gat	1493
Lys Lys Glu Leu His Glu Leu Ala Glu Arg Gln Lys Phe Val Leu Asp	
320 325 330	
ttc cat ttt cct aca ttt gag aga atg aaa tat tta aca aag gag atc	1541
Phe His Phe Pro Thr Phe Glu Arg Met Lys Tyr Leu Thr Lys Glu Ile	
335 340 345	
agc gga cga att tgg gaa aaa tcg att gaa agc gcc gat ttt ctg caa	1589
Ser Gly Arg Ile Trp Glu Lys Ser Ile Glu Ser Ala Asp Phe Leu Gln	
350 355 360	
atc cgc ctt gga acg gga aat gtt gca tct tcg tac caa atc aat ttg	1637
Ile Arg Leu Gly Thr Gly Asn Val Ala Ser Ser Tyr Gln Ile Asn Leu	
365 370 375	
aac ggc gga gat ttg gcc aac cgc gat aca gac cat ctc ctt gaa caa	1685
Asn Gly Gly Asp Leu Ala Asn Arg Asp Thr Asp His Leu Leu Glu Gln	
380 385 390 395	
acg caa aaa atg gaa gag gtc tac aga gag ctg aaa aat gcg ccg atc	1733
Thr Gln Lys Met Glu Glu Val Tyr Arg Glu Leu Lys Asn Ala Pro Ile	
400 405 410	
act gtg aat ctt gcc gaa ggc ccg atg ggc gtc gtc gga aaa ttg tcc	1781
Thr Val Asn Leu Ala Glu Gly Pro Met Gly Val Val Gly Lys Leu Ser	
415 420 425	
gtc gtc aaa aat gaa att cat cag ctt gtc ggc cag ctc gca ttt ttc	1829
Val Val Lys Asn Glu Ile His Gln Leu Val Gly Gln Leu Ala Phe Phe	
430 435 440	
cac agc tat cat gac ttg cgc ttt gtc ttt att ttt gac gaa gcc gag	1877
His Ser Tyr His Asp Leu Arg Phe Val Phe Ile Phe Asp Glu Ala Glu	
445 450 455	
tat caa gaa tgg gaa tgg atg aag tgg ctc ccg cat ttt cag atg cct	1925
Tyr Gln Glu Trp Glu Trp Met Lys Trp Leu Pro His Phe Gln Met Pro	
460 465 470 475	
cat att tat gcg aaa ggg ttt att tac aac gaa cag acg aga gat cag	1973
His Ile Tyr Ala Lys Gly Phe Ile Tyr Asn Glu Gln Thr Arg Asp Gln	
480 485 490	
ctc ctt tca agc ata tat gag att ttg aga gaa cgg gat tta gat gaa	2021
Leu Leu Ser Ser Ile Tyr Glu Ile Leu Arg Glu Arg Asp Leu Asp Glu	
495 500 505	
aac aaa aag aag act ttg ttt aag ccg cac ttt gtg ttt atc atc aca	2069
Asn Lys Lys Lys Thr Leu Phe Lys Pro His Phe Val Phe Ile Ile Thr	
510 515 520	
aat cag cag ctc atc gca gaa cac gtc att tta gaa tat ttg gaa ggc	2117



Asn Gln Gln Leu Ile Ala Glu His Val Ile Leu Glu Tyr Leu Glu Gly	
525 530 535	
aag cag aaa cac ctc gga gtg tcg aca atc gtg gcg gca gag aca aaa	2165
Lys Gln Lys His Leu Gly Val Ser Thr Ile Val Ala Ala Glu Thr Lys	
540 545 550 555	
gaa agc ctg tcc gaa aac att cat acc ctt gtt cgt tat att act gaa	2213
Glu Ser Leu Ser Glu Asn Ile His Thr Leu Val Arg Tyr Ile Thr Glu	
560 565 570	
cag gaa ggc gac att ctg atc aag caa aag aaa gcc gtc cag atc ccg	2261
Gln Glu Gly Asp Ile Leu Ile Lys Gln Lys Lys Ala Val Gln Ile Pro	
575 580 585	
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Phe Gln Leu Asp His His Asn Arg Glu Asp Asn Glu Gln Phe Ser Arg	
590 595 600	
acg ctg aga acg ctt gac cac cag acg ggc atg acg aat tcg att cct	2357
Thr Leu Arg Thr Leu Asp His Gln Thr Gly Met Thr Asn Ser Ile Pro	
605 610 615	
gat acc gta tcg ttt ctc gaa ctg ttc caa gtg aag gaa gtc gat gac	2405
Asp Thr Val Ser Phe Leu Glu Leu Phe Gln Val Lys Glu Val Asp Asp	
620 625 630 635	
atc ggc atc gaa caa aaa tgg atg aca agc gaa tcg gcc aaa tct ttg	2453
Ile Gly Ile Glu Gln Lys Trp Met Thr Ser Glu Ser Ala Lys Ser Leu	
640 645 650	
gcc gtg ccg atc ggc tat aaa gga aaa gac gac att gtt tat tta aac	2501
Ala Val Pro Ile Gly Tyr Lys Gly Lys Asp Asp Ile Val Tyr Leu Asn	
655 660 665	
ctt cac gaa aag gcg cac ggc ccc cac ggg ctg ctt gcc gga acg acc	2549
Leu His Glu Lys Ala His Gly Pro His Gly Leu Leu Ala Gly Thr Thr	
670 675 680	
ggt tcg ggt aaa agt gaa ttt ttg cag act tat att ttg tct ttg gca	2597
Gly Ser Gly Lys Ser Glu Phe Leu Gln Thr Tyr Ile Leu Ser Leu Ala	
685 690 695	
gtt cac ttt cac ccg cat gaa gtc gca ttt ttg cta atc gac tac aaa	2645
Val His Phe His Pro His Glu Val Ala Phe Leu Leu Ile Asp Tyr Lys	
700 705 710 715	
ggg ggc gga atg gcg cag ccg ttc cgg aac att ccg cat ttg ctc gga	2693
Gly Gly Gly Met Ala Gln Pro Phe Arg Asn Ile Pro His Leu Leu Gly	
720 725 730	
acg att act aac att gaa ggc agc aag aac ttc agc aac cgg gcg ctt	2741
Thr Ile Thr Asn Ile Glu Gly Ser Lys Asn Phe Ser Asn Arg Ala Leu	
735 740 745	
gcg tcc att aag agc gag ctg aag aaa agg cag cgg ctc ttt gat cag	2789
Ala Ser Ile Lys Ser Glu Leu Lys Lys Arg Gln Arg Leu Phe Asp Gln	

750	755	760	
tac aaa gtg aac cat atc aac gac tat aca aag ctt tac aaa cag aaa			2837
Tyr Lys Val Asn His Ile Asn Asp Tyr Thr Lys Leu Tyr Lys Gln Lys			
765	770	775	
aaa gcg aaa acg gcg atg ccg cac ctt ttc tta att tca gac gaa ttt			2885
Lys Ala Lys Thr Ala Met Pro His Leu Phe Leu Ile Ser Asp Glu Phe			
780	785	790	795
gcc gag ctg aaa agc gaa gaa ccg gaa ttt atc cgc gag ctt gtc agt			2933
Ala Glu Leu Lys Ser Glu Glu Pro Glu Phe Ile Arg Glu Leu Val Ser			
	800	805	810
gcg gca agg atc ggg cga agc ctc ggg gtg cac tta atc ttg gcg acg			2981
Ala Ala Arg Ile Gly Arg Ser Leu Gly Val His Leu Ile Leu Ala Thr			
	815	820	825
caa aaa ccg ggc ggc atc atc gat gac cag att tgg agc aac tcc aga			3029
Gln Lys Pro Gly Gly Ile Ile Asp Asp Gln Ile Trp Ser Asn Ser Arg			
	830	835	840
ttc aag gtc gcc ttg aag gtg cag gat gcg aat gac agt aaa gag atc			3077
Phe Lys Val Ala Leu Lys Val Gln Asp Ala Asn Asp Ser Lys Glu Ile			
	845	850	855
ctc aaa aac ggg gat gcg gct acc atc acg gta acg ggc cgc ggc tat			3125
Leu Lys Asn Gly Asp Ala Ala Thr Ile Thr Val Thr Gly Arg Gly Tyr			
860	865	870	875
ttg caa gtc ggc aac aac gag gtg tat gaa ctg ttc cag tct gca tgg			3173
Leu Gln Val Gly Asn Asn Glu Val Tyr Glu Leu Phe Gln Ser Ala Trp			
	880	885	890
agc gga gcc cct tac atg gag gac ggc tac ggc aca gag gat gaa gtg			3221
Ser Gly Ala Pro Tyr Met Glu Asp Gly Tyr Gly Thr Glu Asp Glu Val			
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gcg atc gtc aca gat acc gga tta att cct tta tca gat gtt gat gct			3269
Ala Ile Val Thr Asp Thr Gly Leu Ile Pro Leu Ser Asp Val Asp Ala			
	910	915	920
gat cgc gct gcg aaa aaa gag gct gtg acg gaa att tcg gca gtc gtc			3317
Asp Arg Ala Ala Lys Lys Glu Ala Val Thr Glu Ile Ser Ala Val Val			
	925	930	935
gaa caa att gaa cgg att caa gcg gag atg gga atc gag aag ctc ccg			3365
Glu Gln Ile Glu Arg Ile Gln Ala Glu Met Gly Ile Glu Lys Leu Pro			
940	945	950	955
agc cct tgg ctg ccg ccg ctt gaa gaa cgc ata ccg aaa acg cgc tat			3413
Ser Pro Trp Leu Pro Pro Leu Glu Glu Arg Ile Pro Lys Thr Arg Tyr			
	960	965	970
ccg tcg gag gaa gcc gat gcc ttt aac ttt gcc tat atc gat gaa cct			3461
Pro Ser Glu Glu Ala Asp Ala Phe Asn Phe Ala Tyr Ile Asp Glu Pro			
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Glu Lys Gln Ser Gln Glu Pro Ile Ser Tyr Arg Met Met Glu Asp Gly	
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Asn Ile Gly Ile Val Gly Ser Ser Gly Tyr Gly Lys Ser Leu Thr	
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Ala Thr Thr Phe Met Met Ser Phe Ala Glu Gln Tyr Thr Pro Glu	
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Glu Leu His Tyr Tyr Ile Phe Asp Phe Gly Asn Gly Thr Leu Leu	
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Pro Leu Ala Arg Leu Pro His Thr Ala Asp Tyr Phe Leu Met Asp	
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Gln Thr Arg Lys Ile Glu Lys Phe Met Val Arg Ile Lys Ala Glu	
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Ile Glu His Arg Lys Asn Leu Phe Arg Ala Lys Glu Ile Ser His	
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atc aag atg tac aat gcg ctg aat gag gaa aag ctg ccg ttt att	3824
Ile Lys Met Tyr Asn Ala Leu Asn Glu Glu Lys Leu Pro Phe Ile	
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Phe Ile Thr Val Asp Asn Phe Asp Ile Ile Lys Asp Glu Met His	
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1125 1130 1135	
ctt gga att tat tta atc ctg acc gcg aca agg gtc aat gca atc	3959
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1140 1145 1150	
aga cag tcg ctc ttg aac aac ctg aaa acg agg gtt gtc cac tat	4004
Arg Gln Ser Leu Leu Asn Asn Leu Lys Thr Arg Val Val His Tyr	
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Leu Met Asp Gln Ser Glu Ala Tyr Ser Ile Ile Gly Arg Pro Glu	
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Phe Ser Leu Glu Pro Ile Pro Gly Arg Val Ile Ile Asn Lys Glu	
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act gtc gaa ccc gta tac ttt aat ctt gag aaa aat aag cac tgc	4364
Thr Val Glu Pro Val Tyr Phe Asn Leu Glu Lys Asn Lys His Cys	
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ctc att atg ggt cag acg cag cgc gga aaa aca aac gtc atc aag	4409
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Ile Met Leu Glu His Leu Leu Asp His Asp Thr Lys Lys Ile Ala	
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Val Phe Asp Ser Ile Asp Arg Gly Leu Ser Gln Tyr Ala Thr Glu	
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Pro Met Val Phe Ile Val Asp Gly Ile Ser Arg Phe Gln Gln Thr	
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Ile Asp Ala Ser Ile Gln Asp Lys Met Ala Met Phe Met Lys Ser	
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Tyr	Ala	His	Leu	Gly	Phe	His	Phe	Ile	Pro	Ala	Gly	Asn	His	Ser	
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Glu	Phe	Thr	Lys	Gly	Tyr	Asp	Ser	Leu	Thr	Ser	Glu	Val	Lys	Gln	
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Val	Arg	His	Ala	Met	Leu	Leu	Met	Lys	Lys	Ser	Glu	Gln	Asn	Leu	
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Ile	Gln	Leu	Pro	Tyr	Glu	Arg	Gln	Glu	Pro	Glu	Ile	Leu	Pro	Gly	
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Phe	Gly	Tyr	Ile	Val	Glu	Asn	Gly	Lys	Glu	Arg	Lys	Ile	Gln	Ile	
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cct	tta	tgt	gct	gta	gaa	agg	aag	aaa	gcg	aaa	tgacggaaca				4992
Pro	Leu	Cys	Ala	Val	Glu	Arg	Lys	Lys	Ala	Lys					
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			20					25					30		

His Ser Val Thr Ile Lys His Phe Ser Phe Glu Lys Gly Pro Val Thr  
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Leu Glu Lys Gln Lys Asp Ser Asp Ala Leu Asn Val Gln Leu Gly Gly  
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Glu Thr Val Ser Ser Leu Lys Leu Gly Gly Lys Ala Ser Val Gln Ser  
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Gly Ala Glu Gln Leu Thr Leu Phe Leu Ala Glu Glu Ala Asp Ser Val  
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Pro Ala Tyr Tyr Leu Gly Glu Arg Gln Glu Ile Val Ile Ser Ser Leu  
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Asp Gln Glu Ala Asp Val Tyr Phe Asn Glu Thr Asp Ser Phe Phe Gly  
 115 120 125

Glu Lys Gly Thr Phe Ser Phe Ile Arg Leu Asp Gly Gln Trp Asn Val  
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Leu Pro Asn Asp Ala Lys Ile Tyr Leu Asn Gly Glu Glu Val Ser Ala  
 145 150 155 160

Pro Val Ser Val Gln Asn Gly Asp Glu Ile Ala Phe Gly Leu Asn Ile  
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Leu Arg Ile Val Glu Asp Asp Leu Leu Glu Ile Glu Gly Phe Gly Lys  
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Phe Asp Thr Ser Leu Glu Asn Ile Leu Lys Pro Ser Ser Glu Thr Lys  
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Asn Lys Tyr Pro Gln Tyr Arg Arg Pro Pro Arg Met Ile Tyr Asp Leu  
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Pro Asp Glu Lys Val Ser Phe Ser Phe Pro Ala Gln Glu Ser Asp Gly  
 225 230 235 240

Asp Asn Arg Gly Leu Trp Leu Met Ile Leu Pro Pro Leu Val Met Leu  
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Ile Val Met Gly Ile Val Ala Leu Ile Gln Pro Arg Gly Ile Phe Ile



Tyr Glu Ile Leu Arg Glu Arg Asp Leu Asp Glu Asn Lys Lys Lys Thr  
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Leu Phe Lys Pro His Phe Val Phe Ile Ile Thr Asn Gln Gln Leu Ile  
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Ala Glu His Val Ile Leu Glu Tyr Leu Glu Gly Lys Gln Lys His Leu  
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Gly Val Ser Thr Ile Val Ala Ala Glu Thr Lys Glu Ser Leu Ser Glu  
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Asn Ile His Thr Leu Val Arg Tyr Ile Thr Glu Gln Glu Gly Asp Ile  
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Leu Ile Lys Gln Lys Lys Ala Val Gln Ile Pro Phe Gln Leu Asp His  
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His Asn Arg Glu Asp Asn Glu Gln Phe Ser Arg Thr Leu Arg Thr Leu  
595 600 605

Asp His Gln Thr Gly Met Thr Asn Ser Ile Pro Asp Thr Val Ser Phe  
610 615 620

Leu Glu Leu Phe Gln Val Lys Glu Val Asp Asp Ile Gly Ile Glu Gln  
625 630 635 640

Lys Trp Met Thr Ser Glu Ser Ala Lys Ser Leu Ala Val Pro Ile Gly  
645 650 655

Tyr Lys Gly Lys Asp Asp Ile Val Tyr Leu Asn Leu His Glu Lys Ala  
660 665 670

His Gly Pro His Gly Leu Leu Ala Gly Thr Thr Gly Ser Gly Lys Ser  
675 680 685

Glu Phe Leu Gln Thr Tyr Ile Leu Ser Leu Ala Val His Phe His Pro  
690 695 700

His Glu Val Ala Phe Leu Leu Ile Asp Tyr Lys Gly Gly Gly Met Ala  
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Gln Pro Phe Arg Asn Ile Pro His Leu Leu Gly Thr Ile Thr Asn Ile  
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Glu Gly Ser Lys Asn Phe Ser Asn Arg Ala Leu Ala Ser Ile Lys Ser  
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Glu Leu Lys Lys Arg Gln Arg Leu Phe Asp Gln Tyr Lys Val Asn His  
 755 760 765

Ile Asn Asp Tyr Thr Lys Leu Tyr Lys Gln Lys Lys Ala Lys Thr Ala  
 770 775 780

Met Pro His Leu Phe Leu Ile Ser Asp Glu Phe Ala Glu Leu Lys Ser  
 785 790 795 800

Glu Glu Pro Glu Phe Ile Arg Glu Leu Val Ser Ala Ala Arg Ile Gly  
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Arg Ser Leu Gly Val His Leu Ile Leu Ala Thr Gln Lys Pro Gly Gly  
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Ile Ile Asp Asp Gln Ile Trp Ser Asn Ser Arg Phe Lys Val Ala Leu  
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Lys Val Gln Asp Ala Asn Asp Ser Lys Glu Ile Leu Lys Asn Gly Asp  
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Ala Ala Thr Ile Thr Val Thr Gly Arg Gly Tyr Leu Gln Val Gly Asn  
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Asn Glu Val Tyr Glu Leu Phe Gln Ser Ala Trp Ser Gly Ala Pro Tyr  
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Met Glu Asp Gly Tyr Gly Thr Glu Asp Glu Val Ala Ile Val Thr Asp  
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Thr Gly Leu Ile Pro Leu Ser Asp Val Asp Ala Asp Arg Ala Ala Lys  
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Lys Glu Ala Val Thr Glu Ile Ser Ala Val Val Glu Gln Ile Glu Arg  
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Ile Gln Ala Glu Met Gly Ile Glu Lys Leu Pro Ser Pro Trp Leu Pro  
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Pro Leu Glu Glu Arg Ile Pro Lys Thr Arg Tyr Pro Ser Glu Glu Ala  
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Asp Ala Phe Asn Phe Ala Tyr Ile Asp Glu Pro Glu Lys Gln Ser Gln  
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Glu Pro Ile Ser Tyr Arg Met Met Glu Asp Gly Asn Ile Gly Ile Val  
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Ile Phe Asp Phe Gly Asn Gly Thr Leu Leu Pro Leu Ala Arg Leu  
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Pro His Thr Ala Asp Tyr Phe Leu Met Asp Gln Thr Arg Lys Ile  
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Glu Lys Phe Met Val Arg Ile Lys Ala Glu Ile Glu His Arg Lys  
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Asn Leu Phe Arg Ala Lys Glu Ile Ser His Ile Lys Met Tyr Asn  
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Phe Ile Gln Phe Ser Arg Asp Gly Gln Ser Leu Gly Ile Tyr Leu  
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Ile Leu Thr Ala Thr Arg Val Asn Ala Ile Arg Gln Ser Leu Leu  
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Gln Met Phe Met Pro Val	Glu Ala Asp Asn Asp Ile	Glu Leu Phe		
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Glu Gly Ile Lys Ala Asp	Ile Gln Ala Ile Ala Glu	Arg Ser Glu		
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Gly Met Arg Lys Pro Ala	Pro Val Pro Met Leu Pro	Leu Glu Leu		
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Ser Val Thr Gln Phe Val	Arg Asp Tyr Pro Leu Gln	Pro Glu Arg		
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Gly Leu Ile Pro Met Gly	Leu Asp Glu Glu Thr Val	Glu Pro Val		
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Tyr Phe Asn Leu Glu Lys	Asn Lys His Cys Leu Ile	Met Gly Gln		
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Thr Gln Arg Gly Lys Thr	Asn Val Ile Lys Ile Met	Leu Glu His		
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Leu Leu Asp His Asp Thr	Lys Lys Ile Ala Val Phe	Asp Ser Ile		
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Gln Gly Glu Ile Ala Asn	Leu Asp Phe Ser Pro Met	Val Phe Ile		
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Gln Asp Lys Met Ala Met Phe Met Lys Ser Tyr Ala His Leu Gly  
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Tyr Asp Ser Leu Thr Ser Glu Val Lys Gln Val Arg His Ala Met  
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Leu Leu Met Lys Lys Ser Glu Gln Asn Leu Ile Gln Leu Pro Tyr  
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Trp Lys Lys Lys Thr Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu	
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Gln His Leu Thr Glu Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln	
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Tyr	Asp	Asn	Ala	Arg	Lys	Leu	Glu	Arg	Thr	Phe	Gln	Ser	Phe	Gly	Val		
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aag	gcg	aaa	gtc	acc	cag	gtt	cat	ctc	ggc	ccg	gcc	gtc	acg	aaa	tat	1589	
Lys	Ala	Lys	Val	Thr	Gln	Val	His	Leu	Gly	Pro	Ala	Val	Thr	Lys	Tyr		
			350				355					360					
gaa	gtc	tat	cct	gat	gtg	ggc	gtc	aaa	gtc	agc	aaa	att	gtc	aac	tta	1637	
Glu	Val	Tyr	Pro	Asp	Val	Gly	Val	Lys	Val	Ser	Lys	Ile	Val	Asn	Leu		
			365			370					375						
agt	gac	gac	ttg	gct	tta	gcg	ctc	gcg	gcc	aag	gat	atc	cgc	atc	gaa	1685	
Ser	Asp	Asp	Leu	Ala	Leu	Ala	Leu	Ala	Ala	Lys	Asp	Ile	Arg	Ile	Glu		
380					385					390					395		
gcc	ccg	atc	ccc	gga	aaa	tcg	gcg	att	gga	atc	gaa	gtg	ccg	aat	gcg	1733	
Ala	Pro	Ile	Pro	Gly	Lys	Ser	Ala	Ile	Gly	Ile	Glu	Val	Pro	Asn	Ala		
				400					405					410			
gaa	gtg	gcg	atg	gtt	tcc	ttg	aaa	gaa	gtg	ctt	gaa	tcg	aaa	ctg	aat	1781	
Glu	Val	Ala	Met	Val	Ser	Leu	Lys	Glu	Val	Leu	Glu	Ser	Lys	Leu	Asn		
			415					420					425				
gac	cgg	ccg	gat	gca	aag	ctg	atg	atc	ggc	ctc	ggc	cgg	aac	att	tcc	1829	
Asp	Arg	Pro	Asp	Ala	Lys	Leu	Met	Ile	Gly	Leu	Gly	Arg	Asn	Ile	Ser		

430	435	440	
gga gaa gcg gta ttg gca gag ctg aac aaa atg ccc cac ctt ctt gtt Gly Glu Ala Val Leu Ala Glu Leu Asn Lys Met Pro His Leu Leu Val 445 450 455			1877
gca gga gcg acc gga agc ggg aaa agc gtc tgt gtc aac ggg atc att Ala Gly Ala Thr Gly Ser Gly Lys Ser Val Cys Val Asn Gly Ile Ile 460 465 470 475			1925
aca agc att ttg atg agg gca aag ccc cac gaa gtg aag atg atg atg Thr Ser Ile Leu Met Arg Ala Lys Pro His Glu Val Lys Met Met Met 480 485 490			1973
att gat ccg aaa atg gtc gag ctc aat gtc tac aac ggg att ccg cat Ile Asp Pro Lys Met Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His 495 500 505			2021
ttg ctc gct ccc gtc gtg aca gac ccg aaa aaa gca tcg cag gct ttg Leu Leu Ala Pro Val Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu 510 515 520			2069
aag aaa gtc gtc aac gaa atg gag cgg cgc tac gaa ttg ttt tct cac Lys Lys Val Val Asn Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His 525 530 535			2117
acg gga acg aga aat atc gaa ggg tat aac gac tat att aaa cgg atg Thr Gly Thr Arg Asn Ile Glu Gly Tyr Asn Asp Tyr Ile Lys Arg Met 540 545 550 555			2165
aat gcc gca gaa gaa gca aag cag ccg gag ctt cca tac atc att gtg Asn Ala Ala Glu Glu Ala Lys Gln Pro Glu Leu Pro Tyr Ile Ile Val 560 565 570			2213
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gaa gac tcg atc aca agg ctt tcg caa atg gcc agg gcg gcg ggc atc Glu Asp Ser Ile Thr Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile 590 595 600			2309
cac ctg atc att gcg acg cag agg cct tcg gtc gat gtt atc aca ggg His Leu Ile Ile Ala Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly 605 610 615			2357
gtc att aaa gcc aac att ccg tca agg atc gct ttc agc gta tcg tct Val Ile Lys Ala Asn Ile Pro Ser Arg Ile Ala Phe Ser Val Ser Ser 620 625 630 635			2405
cag acc gac tcc agg acg att ctt gat atg gga ggc gct gaa aaa ctt Gln Thr Asp Ser Arg Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu 640 645 650			2453
ctc ggc aga ggg gac atg ctg ttt ctc cct gtc ggc gcc aat aaa ccg Leu Gly Arg Gly Asp Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro 655 660 665			2501

ctc cgc gtt caa ggt gcc ttt ctg tca gac gaa gaa gtt gaa aaa gtt Leu Arg Val Gln Gly Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val 670 675 680	2549
gtc gat cac gtc atc agc cag caa aaa gcc caa tac caa gaa gaa atg Val Asp His Val Ile Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met 685 690 695	2597
att cca gaa gag acg cag gaa acg gtc agc gaa gtg aca gac gac ctt Ile Pro Glu Glu Thr Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu 700 705 710 715	2645
tat gac gaa gcg gtc gca ctt gtg gtc agc atg cag acg gct tct gta Tyr Asp Glu Ala Val Ala Leu Val Val Ser Met Gln Thr Ala Ser Val 720 725 730	2693
tcc atg ctg caa agg aga ttc cgc atc ggc tat aca aga gcg gcg cgg Ser Met Leu Gln Arg Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg 735 740 745	2741
ctt atc gat gcc atg gaa gag cgg gga atc gtc ggc cca tat gaa gga Leu Ile Asp Ala Met Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly 750 755 760	2789
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tct tct tgagaagaga gttcttgttt aacataattt cattatgtaa actaaaaaac Ser Ser 780	2893
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<400> 191



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 Ile Ser Ile Ile Ala Val Leu Gln Leu Gly Val Ala Gly Gln Thr Phe  
 35 40 45  
 Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp Phe Ile Leu Cys Leu  
 50 55 60  
 Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe Trp Lys Lys Lys Thr  
 65 70 75 80  
 Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu Tyr Cys Ile Ile Ala  
 85 90 95  
 Ser Met Leu Leu Leu Ser His Val Gln Leu Phe Gln His Leu Thr Glu  
 100 105 110  
 Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln Asn Thr Trp Glu Leu  
 115 120 125  
 Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser Pro Asp Leu Gly Gly  
 130 135 140  
 Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser Tyr Phe Leu Phe Ala  
 145 150 155 160  
 Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu Ile Leu Ile Gly Leu  
 165 170 175  
 Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr Leu Ile Lys Trp Met  
 180 185 190  
 Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp Gln Ala Phe Leu Ala  
 195 200 205  
 Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys Lys Lys Ser Gly Lys  
 210 215 220  
 Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser Glu Glu Pro Val Gln

225		230		235		240
Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln Ser Glu Pro Ile Ile						
	245			250		255
Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu Val Gln Ala Tyr Glu						
	260			265		270
Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu Pro Glu Ile Gly Glu						
	275			280		285
Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr Phe Thr Glu Leu Glu						
	290			295		300
Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu Leu Asp Asp Pro Lys						
305		310		315		320
His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile Tyr Asp Asn Ala Arg						
	325			330		335
Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val Lys Ala Lys Val Thr						
	340			345		350
Gln Val His Leu Gly Pro Ala Val Thr Lys Tyr Glu Val Tyr Pro Asp						
	355			360		365
Val Gly Val Lys Val Ser Lys Ile Val Asn Leu Ser Asp Asp Leu Ala						
	370			375		380
Leu Ala Leu Ala Ala Lys Asp Ile Arg Ile Glu Ala Pro Ile Pro Gly						
385		390		395		400
Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala Glu Val Ala Met Val						
	405			410		415
Ser Leu Lys Glu Val Leu Glu Ser Lys Leu Asn Asp Arg Pro Asp Ala						
	420			425		430
Lys Leu Met Ile Gly Leu Gly Arg Asn Ile Ser Gly Glu Ala Val Leu						
	435			440		445
Ala Glu Leu Asn Lys Met Pro His Leu Leu Val Ala Gly Ala Thr Gly						
	450			455		460

Ser Gly Lys Ser Val Cys Val Asn Gly Ile Ile Thr Ser Ile Leu Met  
 465 470 475 480

Arg Ala Lys Pro His Glu Val Lys Met Met Met Ile Asp Pro Lys Met  
 485 490 495

Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His Leu Leu Ala Pro Val  
 500 505 510

Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu Lys Lys Val Val Asn  
 515 520 525

Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His Thr Gly Thr Arg Asn  
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Ile Glu Gly Tyr Asn Asp Tyr Ile Lys Arg Met Asn Ala Ala Glu Glu  
 545 550 555 560

Ala Lys Gln Pro Glu Leu Pro Tyr Ile Ile Val Ile Val Asp Glu Leu  
 565 570 575

Ala Asp Leu Met Met Val Ala Ser Ser Asp Val Glu Asp Ser Ile Thr  
 580 585 590

Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile His Leu Ile Ile Ala  
 595 600 605

Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly Val Ile Lys Ala Asn  
 610 615 620

Ile Pro Ser Arg Ile Ala Phe Ser Val Ser Ser Gln Thr Asp Ser Arg  
 625 630 635 640

Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu Leu Gly Arg Gly Asp  
 645 650 655

Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro Leu Arg Val Gln Gly  
 660 665 670

Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val Val Asp His Val Ile  
 675 680 685

Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met Ile Pro Glu Glu Thr  
690 695 700

Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu Tyr Asp Glu Ala Val  
705 710 715 720

Ala Leu Val Val Ser Met Gln Thr Ala Ser Val Ser Met Leu Gln Arg  
725 730 735

Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg Leu Ile Asp Ala Met  
740 745 750

Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly Ser Lys Pro Arg Glu  
755 760 765

Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu Ser Ser  
770 775 780